

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 13, 2001, 12:00:19 ; Search time 174.34 Seconds  
(without alignments)  
12.741 Million cell updates/sec

Title: US-09-424-080A-2

Perfect score: 11

Sequence: A-LXXXXXX 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 36232

Minimum DB seq length: 8

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA Main:

- 1: /cgn2\_6/ptodata/2/paa/PCTUS00000903
- 2: /cgn2\_6/ptodata/2/paa/US06\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/paa/US07\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/paa/US08\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/paa/US081\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/paa/US082\_COMB.pep.\*
- 7: /cgn2\_6/ptodata/2/paa/US083\_COMB.pep.\*
- 8: /cgn2\_6/ptodata/2/paa/US084\_COMB.pep.\*
- 9: /cgn2\_6/ptodata/2/paa/US085\_COMB.pep.\*
- 10: /cgn2\_6/ptodata/2/paa/US086\_COMB.pep.\*
- 11: /cgn2\_6/ptodata/2/paa/US087\_COMB.pep.\*
- 12: /cgn2\_6/ptodata/2/paa/US088\_COMB.pep.\*
- 13: /cgn2\_6/ptodata/2/paa/US089\_COMB.pep.\*
- 14: /cgn2\_6/ptodata/2/paa/US090\_COMB.pep.\*
- 15: /cgn2\_6/ptodata/2/paa/US091\_COMB.pep.\*
- 16: /cgn2\_6/ptodata/2/paa/US092\_COMB.pep.\*
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- 19: /cgn2\_6/ptodata/2/paa/US095\_COMB.pep.\*
- 20: /cgn2\_6/ptodata/2/paa/US096\_COMB.pep.\*
- 21: /cgn2\_6/ptodata/2/paa/US097\_COMB.pep.\*
- 22: /cgn2\_6/ptodata/2/paa/US098\_COMB.pep.\*
- 23: /cgn2\_6/ptodata/2/paa/US099\_COMB.pep.\*
- 24: /cgn2\_6/ptodata/2/paa/US60\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	DB ID	Description
1	4	36.4	8 1	PCT-US00-00903-105
2	4	36.4	8 1	PCT-US00-01012-48
3	4	36.4	8 1	PCT-US00-01602-98
4	4	36.4	8 1	PCT-US00-01602-104
5	4	36.4	8 1	PCT-US00-01602-154
6	4	36.4	8 1	PCT-US00-01602-159
7	4	36.4	8 1	PCT-US00-01602-161
8	4	36.4	8 1	PCT-US00-01602-162
9	4	36.4	8 1	PCT-US00-01602-162

10	4	36.4	8 1	PCT-US00-01602-186
11	4	36.4	8 1	PCT-US00-03559-2
12	4	36.4	8 1	PCT-US00-03559-10
13	4	36.4	8 1	PCT-US00-03559-11
14	4	36.4	8 1	PCT-US00-03559-12
15	4	36.4	8 1	PCT-US00-03559-16
16	4	36.4	8 1	PCT-US00-03559-17
17	4	36.4	8 1	PCT-US00-03864-16
18	4	36.4	8 1	PCT-US00-04565-2
19	4	36.4	8 1	PCT-US00-06043-67
20	4	36.4	8 1	PCT-US00-06166-1
21	4	36.4	8 1	PCT-US00-06765-85
22	4	36.4	8 1	PCT-US00-06765-85
23	4	36.4	8 1	PCT-US00-06823-90
24	4	36.4	8 1	PCT-US00-06823-121
25	4	36.4	8 1	PCT-US00-06823-122
26	4	36.4	8 1	PCT-US00-06828-93
27	4	36.4	8 1	PCT-US00-06830-86
28	4	36.4	8 1	PCT-US00-07507-109
29	4	36.4	8 1	PCT-US00-07578B-126
30	4	36.4	8 1	PCT-US00-07579-103
31	4	36.4	8 1	PCT-US00-07686-46
32	4	36.4	8 1	PCT-US00-07725-96
33	4	36.4	8 1	PCT-US00-08347-3
34	4	36.4	8 1	PCT-US00-08561-45
35	4	36.4	8 1	PCT-US00-08746-6
36	4	36.4	8 1	PCT-US00-08979-261
37	4	36.4	8 1	PCT-US00-09068-83
38	4	36.4	8 1	PCT-US00-09069-74
39	4	36.4	8 1	PCT-US00-09069-74
40	4	36.4	8 1	PCT-US00-09465-7
41	4	36.4	8 1	PCT-US00-10344-25
42	4	36.4	8 1	PCT-US00-12788-161
43	4	36.4	8 1	PCT-US00-13292-35
44	4	36.4	8 1	PCT-US00-14687-6
45	4	36.4	8 24	US-60-185-205-142

## ALIGNMENTS

RESULT 1  
PCT-US00-00903-105  
; Sequence 105, Application PC/TUS00000903  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: P2036.PCT  
; FILE REFERENCE: P2036.PCT  
; CURRENT APPLICATION NUMBER: PCT/US00/00903  
; EARLIER FILING DATE: 2000-01-18  
; EARLIER FILING DATE: 1999-01-19  
; NUMBER OF SEQ ID NOS: 144  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 105  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US00-00903-105

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 L 1  
Db 1 L 1

RESULT 2  
PCT-US00-01012-48  
; Sequence 48, Application PC/TUS00001012

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; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; TITLE OF INVENTION: Methods for Inhibiting Tumor Metastasis, and Peptides
; FILE REFERENCE: FP-LJ 3865
; CURRENT FILING DATE: 2000-01-14
; EARLIER APPLICATION NUMBER: 09/232,484
; PRIOR FILING DATE: 1999-01-05
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(2)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (5)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (7)..(8)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
; OTHER INFORMATION: Sequence
PCT-US00-01012-48
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Query Match          36.4%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 L 1
   |
Db 4 L 4
```

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RESULT 3
PCT-US00-01602-4
; Sequence 4, Application PC/TUS0001602
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; TITLE OF INVENTION: Homing Pro-Apoptotic Conjugates and Methods of Using
; FILE REFERENCE: FP-LJ 3866
; CURRENT APPLICATION NUMBER: PCT/US00/01602
; CURRENT FILING DATE: 2000-01-21
; PRIOR FILING DATE: 1999-01-22
; NUMBER OF SEQ ID NOS: 235
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
PCT-US00-01602-4
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Query Match          36.4%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 L 1
   |
Db 2 L 2
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RESULT 4
PCT-US00-01602-98
; Sequence 98, Application PC/TUS0001602
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; TITLE OF INVENTION: Homing Pro-Apoptotic Conjugates and Methods of Using
; FILE REFERENCE: FP-LJ 3866
; CURRENT APPLICATION NUMBER: PCT/US00/01602
; CURRENT FILING DATE: 2000-01-21
; PRIOR FILING DATE: 1999-01-22
; NUMBER OF SEQ ID NOS: 235
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
PCT-US00-01602-98
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```
Query Match          36.4%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 L 1
   |
Db 6 L 6
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```
RESULT 5
PCT-US00-01602-104
; Sequence 104, Application PC/TUS0001602
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; TITLE OF INVENTION: Homing Pro-Apoptotic Conjugates and Methods of Using
; FILE REFERENCE: FP-LJ 3866
; CURRENT APPLICATION NUMBER: PCT/US00/01602
; CURRENT FILING DATE: 2000-01-21
; PRIOR FILING DATE: 1999-01-22
; NUMBER OF SEQ ID NOS: 235
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
PCT-US00-01602-104
```

```
Query Match          36.4%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 L 1
   |
Db 4 L 4
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```
RESULT 6
PCT-US00-01602-154
; Sequence 154, Application PC/TUS0001602
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
```

;; TITLE OF INVENTION: Homing Pro-Apoptotic Conjugates and Methods of Using  
;; FILE REFERENCE: Same  
;; CURRENT APPLICATION NUMBER: PCT/US00/01602  
;; PRIOR FILING DATE: 2000-01-21  
;; PRIOR APPLICATION NUMBER: US 09/235,902  
;; NUMBER OF SEQ ID NOS: 235  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 154  
;; LENGTH: 8  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;; OTHER INFORMATION: Peptide  
PCT-US00-01602-154

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
DB 5 L 5

RESULT 7  
PCT-US00-01602-159  
;; Sequence 159, Application PC/TUS00001602  
;; GENERAL INFORMATION:  
;; APPLICANT: The Burnham Institute  
;; TITLE OF INVENTION: Homing Pro-Apoptotic Conjugates and Methods of Using  
;; FILE REFERENCE: Same  
;; CURRENT APPLICATION NUMBER: PCT/US00/01602  
;; CURRENT FILING DATE: 2000-01-21  
;; PRIOR FILING DATE: 1999-01-22  
;; NUMBER OF SEQ ID NOS: 235  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 159  
;; LENGTH: 8  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;; OTHER INFORMATION: Peptide  
PCT-US00-01602-159

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
DB 4 L 4

RESULT 8  
PCT-US00-01602-161  
;; Sequence 161, Application PC/TUS00001602  
;; GENERAL INFORMATION:  
;; APPLICANT: The Burnham Institute  
;; TITLE OF INVENTION: Homing Pro-Apoptotic Conjugates and Methods of Using  
;; FILE REFERENCE: Same  
;; CURRENT APPLICATION NUMBER: PCT/US00/01602  
;; CURRENT FILING DATE: 2000-01-21  
;; PRIOR FILING DATE: 1999-01-22

;; NUMBER OF SEQ ID NOS: 235  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 161  
;; LENGTH: 8  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;; OTHER INFORMATION: Peptide  
PCT-US00-01602-161

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
DB 3 L 3

RESULT 9  
PCT-US00-01602-162  
;; Sequence 162, Application PC/TUS00001602  
;; GENERAL INFORMATION:  
;; APPLICANT: The Burnham Institute  
;; TITLE OF INVENTION: Homing Pro-Apoptotic Conjugates and Methods of Using  
;; FILE REFERENCE: Same  
;; CURRENT APPLICATION NUMBER: PCT/US00/01602  
;; CURRENT FILING DATE: 2000-01-21  
;; PRIOR FILING DATE: 1999-01-22  
;; NUMBER OF SEQ ID NOS: 235  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 162  
;; LENGTH: 8  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;; OTHER INFORMATION: Peptide  
PCT-US00-01602-162

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
DB 3 L 3

RESULT 10  
PCT-US00-01602-186  
;; Sequence 186, Application PC/TUS00001602  
;; GENERAL INFORMATION:  
;; APPLICANT: The Burnham Institute  
;; TITLE OF INVENTION: Homing Pro-Apoptotic Conjugates and Methods of Using  
;; FILE REFERENCE: Same  
;; CURRENT APPLICATION NUMBER: PCT/US00/01602  
;; CURRENT FILING DATE: 2000-01-21  
;; PRIOR FILING DATE: 1999-01-22  
;; NUMBER OF SEQ ID NOS: 235  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 186  
;; LENGTH: 8  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Peptide  
 PCT-US00-01602-186

Query Match 36.4%; Score 4; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1  
 Db 3 L 3

RESULT 11  
 PCT-US00-03559-2

; Sequence 2, Application PC/TUS00003559A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MUKHERJEE, RAMA  
 ; APPLICANT: JAGGI, MANU  
 ; APPLICANT: PRASAD, SUDHANAND  
 ; APPLICANT: BURMAN, ANAND C  
 ; APPLICANT: RAJENDRAN, PRAVEEN  
 ; APPLICANT: MATHUR, ARCHANA  
 ; APPLICANT: SINGH, ANU T  
 ; TITLE OF INVENTION: ANTIANGIOGENIC DRUGS  
 ; FILE REFERENCE: 09/248,381  
 ; CURRENT APPLICATION NUMBER: PCT/US00/03559A  
 ; PRIOR FILING DATE: 2000-02-11  
 ; PRIOR FILING DATE: 09/248,381  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 8

TYPE: PRT  
 ORGANISM: Artificial Sequence

; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: This peptide  
 ; OTHER INFORMATION: was synthetically generated.

PCT-US00-03559-2

Query Match 36.4%; Score 4; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1  
 Db 1 L 1

RESULT 12  
 PCT-US00-03559-10

; Sequence 10, Application PC/TUS00003559A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MUKHERJEE, RAMA  
 ; APPLICANT: JAGGI, MANU  
 ; APPLICANT: PRASAD, SUDHANAND  
 ; APPLICANT: BURMAN, ANAND C  
 ; APPLICANT: RAJENDRAN, PRAVEEN  
 ; APPLICANT: MATHUR, ARCHANA  
 ; APPLICANT: SINGH, ANU T  
 ; TITLE OF INVENTION: ANTIANGIOGENIC DRUGS

; FILE REFERENCE: 09/248,381  
 ; CURRENT APPLICATION NUMBER: PCT/US00/03559A  
 ; PRIOR FILING DATE: 2000-02-11  
 ; PRIOR FILING DATE: 09/248,381  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 10  
 ; LENGTH: 8

; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: This peptide  
 ; OTHER INFORMATION: was synthetically generated.  
 ; NAME/KEY: MOD\_RES  
 ; LOCATION: (6)  
 ; OTHER INFORMATION: /product=D-tyrosine/label=D-Tyr  
 PCT-US00-03559-10

Query Match 36.4%; Score 4; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1  
 Db 1 L 1

RESULT 13

PCT-US00-03559-11  
 ; Sequence 11, Application PC/TUS00003559A  
 ; GENERAL INFORMATION:

; APPLICANT: MUKHERJEE, RAMA  
 ; APPLICANT: JAGGI, MANU  
 ; APPLICANT: PRASAD, SUDHANAND  
 ; APPLICANT: BURMAN, ANAND C  
 ; APPLICANT: RAJENDRAN, PRAVEEN  
 ; APPLICANT: MATHUR, ARCHANA  
 ; APPLICANT: SINGH, ANU T  
 ; TITLE OF INVENTION: ANTIANGIOGENIC DRUGS

; FILE REFERENCE: 09/248,381  
 ; CURRENT APPLICATION NUMBER: PCT/US00/03559A  
 ; CURRENT FILING DATE: 2000-02-11  
 ; PRIOR FILING DATE: 09/248,381  
 ; PRIOR FILING DATE: 1999-02-11  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 11  
 ; LENGTH: 8

TYPE: PRT  
 ORGANISM: Artificial Sequence

; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: This peptide  
 ; OTHER INFORMATION: was synthetically generated.

; NAME/KEY: MOD\_RES

; LOCATION: (7)  
 ; OTHER INFORMATION: /product=D-leucine/label=D-Leu  
 PCT-US00-03559-11

Query Match 36.4%; Score 4; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1  
 Db 1 L 1

RESULT 14

PCT-US00-03559-12  
 ; Sequence 12, Application PC/TUS00003559A  
 ; GENERAL INFORMATION:

; APPLICANT: MUKHERJEE, RAMA  
 ; APPLICANT: JAGGI, MANU  
 ; APPLICANT: PRASAD, SUDHANAND  
 ; APPLICANT: BURMAN, ANAND C  
 ; APPLICANT: RAJENDRAN, PRAVEEN  
 ; APPLICANT: MATHUR, ARCHANA  
 ; APPLICANT: SINGH, ANU T  
 ; TITLE OF INVENTION: ANTIANGIOGENIC DRUGS



FILE REFERENCE: 09/248,381  
CURRENT APPLICATION NUMBER: PCT/US00/03559A  
CURRENT FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: 09/248,381  
PRIOR FILING DATE: 1999-02-11  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 12  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: This peptide  
OTHER INFORMATION: was synthetically generated.  
NAME/KEY: MOD\_RES  
LOCATION: (3)  
OTHER INFORMATION: /product=D-tyrosine/label=D-Tyr  
NAME/KEY: MOD\_RES  
LOCATION: (7)  
OTHER INFORMATION: /product=D-leucine/label=D-Leu  
PCT-US00-03559-12

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
Db 1 L 1

RESULT 15  
PCT-US00-03559-16  
Sequence 16, Application PC/TUS0003559A  
GENERAL INFORMATION:  
APPLICANT: MUKHERJEE, RAMA  
APPLICANT: JAGGI, MANU  
APPLICANT: PRASAD, SUDHANAND  
APPLICANT: BURMAN, ANAND C  
APPLICANT: RAJENDRAN, PRAVEEN  
APPLICANT: MATHUR, ARCHANA  
APPLICANT: SINGH, ANU T  
TITLE OF INVENTION: ANTIANGIOGENIC DRUGS  
FILE REFERENCE: 09/248,381  
CURRENT APPLICATION NUMBER: PCT/US00/03559A  
CURRENT FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: 09/248,381  
PRIOR FILING DATE: 1999-02-11  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 16  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: This peptide  
OTHER INFORMATION: was synthetically generated.  
NAME/KEY: MOD\_RES  
LOCATION: (1)  
OTHER INFORMATION: /product=D-phenylalanine/label=D-Phe;  
NAME/KEY: MOD\_RES  
LOCATION: (4)  
OTHER INFORMATION: /product=2-amino-isobutyric acid/label=Alb  
PCT-US00-03559-16

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
Db 1 L 1

Db 8 L 8

Search completed: December 13, 2001, 12:00:19  
Job time: 282 sec

GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: December 13, 2001, 12:00:34 ; Search time 9.12 Seconds  
(without alignments)  
10.106 Million cell updates/sec

Title: US-09-424-080A-2

Perfect score: 11

Sequence: 1. LXXXXXX 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 61579 seqs, 11521160 residues

Total number of hits satisfying chosen parameters: 876

Minimum DB seq length: 8

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2.6/ptodata/1/paa/PCT\_NEW\_COMB.pcp:\*\*
- 2: /cgn2.6/ptodata/1/paa/US05\_NEW\_COMB.pcp:\*\*
- 3: /cgn2.6/ptodata/1/paa/US07\_NEW\_COMB.pcp:\*\*
- 4: /cgn2.6/ptodata/1/paa/US08\_NEW\_COMB.pcp:\*\*
- 5: /cgn2.6/ptodata/1/paa/US09\_NEW\_COMB.pcp:\*\*
- 6: /cgn2.6/ptodata/1/paa/US60\_NEW\_COMB.pcp:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query % Match	Score	Length	DB ID	Description
1	4	36.4	8	1	PCT-US00-03561-28
2	4	36.4	8	1	PCT-US01-17103-43
3	4	36.4	8	1	PCT-US00-33903-18
4	4	36.4	8	1	PCT-US01-27692A-103
5	4	36.4	8	1	PCT-US01-27692A-114
6	4	36.4	8	1	PCT-US01-27692A-241
7	4	36.4	8	1	PCT-US01-28124A-6
8	4	36.4	8	1	PCT-US01-28124A-41
9	4	36.4	8	1	PCT-US01-28124A-42
10	4	36.4	8	1	PCT-US01-28124A-43
11	4	36.4	8	1	PCT-US01-28124A-44
12	4	36.4	8	1	PCT-US01-28124A-46
13	4	36.4	8	1	PCT-US01-28124A-50
14	4	36.4	8	1	PCT-US01-28124A-56
15	4	36.4	8	1	PCT-US01-28124A-59
16	4	36.4	8	1	PCT-US01-28124A-128
17	4	36.4	8	1	PCT-US01-28124A-132
18	4	36.4	8	1	PCT-US01-28124A-133
19	4	36.4	8	1	PCT-US01-28124A-134
20	4	36.4	8	1	PCT-US01-28124A-135
21	4	36.4	8	1	PCT-US01-28124A-262
22	4	36.4	8	4	US-08-453-623-51
23	4	36.4	8	4	US-08-816-454B-4
24	4	36.4	8	4	US-08-816-454B-103
25	4	36.4	8	4	US-08-816-454B-152
26	4	36.4	8	4	US-08-816-454B-153
27	4	36.4	8	4	US-08-816-454B-155

28	4	36.4	8	4	US-08-816-454B-156
29	4	36.4	8	4	US-08-816-454B-157
30	4	36.4	8	4	US-08-816-454B-158
31	4	36.4	8	4	US-08-816-454B-159
32	4	36.4	8	4	US-08-816-454B-160
33	4	36.4	8	4	US-08-816-454B-170
34	4	36.4	8	4	US-08-816-454B-180
35	4	36.4	8	4	US-08-816-454B-189
36	4	36.4	8	4	US-08-974-685-69
37	4	36.4	8	4	US-08-974-685-72
38	4	36.4	8	4	US-08-974-685-81
39	4	36.4	8	4	US-08-974-685-83
40	4	36.4	8	4	US-08-974-685-89
41	4	36.4	8	4	US-08-974-685-90
42	4	36.4	8	4	US-08-974-685-92
43	4	36.4	8	4	US-08-974-685-95
44	4	36.4	8	4	US-08-974-685-110
45	4	36.4	8	5	US-09-938-671-161

## ALIGNMENTS

RESULT 1  
PCT-US00-03561-28  
; Sequence 28, Application PC/TUS0003561  
; GENERAL INFORMATION:  
; APPLICANT: The General Hospital Corporation  
; TITLE OF INVENTION: Compositions and Methods for Modulating TGF-B Signaling  
; FILE REFERENCE: 11275/96218  
; CURRENT APPLICATION NUMBER: PCT/US00/03561  
; CURRENT FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US00-03561-28

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
Db 5 L 5

RESULT 2  
PCT-US01-17103-43  
; Sequence 43, Application PC/TUS0117103  
; GENERAL INFORMATION:  
; APPLICANT: University of Massachusetts  
; TITLE OF INVENTION: INTRAFAGELLAR TRANSPORT  
; FILE REFERENCE: 07917-145W01  
; CURRENT APPLICATION NUMBER: PCT/US01/17103  
; CURRENT FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: US 60/206,923  
; PRIOR FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 43  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Chlamydomonas reinhardtii  
PCT-US01-17103-43

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
Db 1 L 1

RESULT 3  
PCT-US00-33903-18  
; Sequence 18, Application PC/TUS0033903  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSTON-WILSON, NANCY L.  
; APPLICANT: SIMS, CHRISTINA D.  
; APPLICANT: HOFMANN, JEAN-PAUL  
; APPLICANT: ANDERSON, N. LEIGH  
; APPLICANT: SHORE, ANDREW D.  
; APPLICANT: YOLKEN, ROBERT H.  
; APPLICANT: TORREY, E. FULLER  
; TITLE OF INVENTION: BRAIN PROTEIN MARKERS  
; FILE REFERENCE: 41169  
; CURRENT APPLICATION NUMBER: PCT/US00/33903  
; CURRENT FILING DATE: 2001-07-12  
; PRIOR APPLICATION NUMBER: 60/172,286  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US00-33903-18

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
Db 5 L 5

RESULT 4  
PCT-US01-27692A-103  
; Sequence 103, Application PC/TUS0127692A  
; GENERAL INFORMATION:  
; APPLICANT: Board of Regents, The University of Texas System  
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display  
; FILE REFERENCE: 005774.P003PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/27692A  
; CURRENT FILING DATE: 2001-09-07  
; NUMBER OF SEQ ID NOS: 251  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 103  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: (1)..(8)  
; OTHER INFORMATION: synthetic construct  
PCT-US01-27692A-103

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
Db 3 L 3

RESULT 5

PCT-US01-27692A-114  
; Sequence 114, Application PC/TUS0127692A  
; GENERAL INFORMATION:  
; APPLICANT: Board of Regents, The University of Texas System  
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display  
; FILE REFERENCE: 005774.P003PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/27692A  
; CURRENT FILING DATE: 2001-09-07  
; NUMBER OF SEQ ID NOS: 251  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 114  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: (1)..(8)  
; OTHER INFORMATION: synthetic construct  
PCT-US01-27692A-114

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
Db 8 L 8

RESULT 6  
PCT-US01-27692A-241  
; Sequence 241, Application PC/TUS0127692A  
; GENERAL INFORMATION:  
; APPLICANT: Board of Regents, The University of Texas System  
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display  
; FILE REFERENCE: 005774.P003PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/27692A  
; CURRENT FILING DATE: 2001-09-07  
; NUMBER OF SEQ ID NOS: 251  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 241  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: (1)..(8)  
; OTHER INFORMATION: synthetic construct  
PCT-US01-27692A-241

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
Db 2 L 2

RESULT 7  
PCT-US01-28124A-6  
; Sequence 6, Application PC/TUS0128124A  
; GENERAL INFORMATION:  
; APPLICANT: Board of Regents, The University of Texas System  
; TITLE OF INVENTION: Biopanning and Rapid Analysis of Selective Interactive Ligands  
; FILE REFERENCE: 005774.P004PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/28124A  
; CURRENT FILING DATE: 2001-09-07  
; NUMBER OF SEQ ID NOS: 289  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6

; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: (1)..(8)  
; OTHER INFORMATION: synthetic construct  
PCT-US01-28124A-6

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
|  
Db 7 L 7

RESULT 8  
PCT-US01-28124A-41  
; Sequence 41, Application PC/TUS0128124A  
; GENERAL INFORMATION:  
; APPLICANT: Board of Regents, The University of Texas System  
; TITLE OF INVENTION: Biopanning and Rapid Analysis of Selective Interactive Ligands (E  
; FILE REFERENCE: 005774.P004PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/28124A  
; CURRENT FILING DATE: 2001-09-07  
; NUMBER OF SEQ ID NOS: 289  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 41  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: (1)..(8)  
; OTHER INFORMATION: synthetic construct  
PCT-US01-28124A-41

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
|  
Db 6 L 6

RESULT 9  
PCT-US01-28124A-42  
; Sequence 42, Application PC/TUS0128124A  
; GENERAL INFORMATION:  
; APPLICANT: Board of Regents, The University of Texas System  
; TITLE OF INVENTION: Biopanning and Rapid Analysis of Selective Interactive Ligands (E  
; FILE REFERENCE: 005774.P004PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/28124A  
; CURRENT FILING DATE: 2001-09-07  
; NUMBER OF SEQ ID NOS: 289  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 42  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: (1)..(8)  
; OTHER INFORMATION: synthetic construct  
PCT-US01-28124A-42

Query Match 36.4%; Score 4; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 4.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
|  
Db 2 L 2

RESULT 10  
PCT-US01-28124A-43  
; Sequence 43, Application PC/TUS0128124A  
; GENERAL INFORMATION:  
; APPLICANT: Board of Regents, The University of Texas System  
; TITLE OF INVENTION: Biopanning and Rapid Analysis of Selective Interactive Ligands  
; FILE REFERENCE: 005774.P004PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/28124A  
; CURRENT FILING DATE: 2001-09-07  
; NUMBER OF SEQ ID NOS: 289  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 43  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: (1)..(8)  
; OTHER INFORMATION: synthetic construct  
PCT-US01-28124A-43

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
|  
Db 2 L 2

RESULT 11  
PCT-US01-28124A-44  
; Sequence 44, Application PC/TUS0128124A  
; GENERAL INFORMATION:  
; APPLICANT: Board of Regents, The University of Texas System  
; TITLE OF INVENTION: Biopanning and Rapid Analysis of Selective Interactive Ligands  
; FILE REFERENCE: 005774.P004PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/28124A  
; CURRENT FILING DATE: 2001-09-07  
; NUMBER OF SEQ ID NOS: 289  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 44  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: (1)..(8)  
; OTHER INFORMATION: synthetic construct  
PCT-US01-28124A-44

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
|  
Db 3 L 3

RESULT 12  
PCT-US01-28124A-46  
; Sequence 46, Application PC/TUS0128124A

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; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Biopanning and Rapid Analysis of Selective Interactive Ligands (E
; FILE REFERENCE: 005774.P004PCT
; CURRENT APPLICATION NUMBER: PCT/US01/28124A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(8)
; OTHER INFORMATION: synthetic construct
PCT-US01-28124A-46

Query Match          36.4%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
   |
Db 5 L 5

RESULT 13
PCT-US01-28124A-50
; Sequence 50, Application PC/TUS0128124A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Biopanning and Rapid Analysis of Selective Interactive Ligands (E
; FILE REFERENCE: 005774.P004PCT
; CURRENT APPLICATION NUMBER: PCT/US01/28124A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(8)
; OTHER INFORMATION: synthetic construct
PCT-US01-28124A-50

Query Match          36.4%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
   |
Db 2 L 2

RESULT 14
PCT-US01-28124A-56
; Sequence 56, Application PC/TUS0128124A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Biopanning and Rapid Analysis of Selective Interactive Ligands (E
; FILE REFERENCE: 005774.P004PCT
; CURRENT APPLICATION NUMBER: PCT/US01/28124A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 8
; TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(8)
; OTHER INFORMATION: synthetic construct
PCT-US01-28124A-56

Query Match          36.4%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
   |
Db 2 L 2

RESULT 15
PCT-US01-28124A-59
; Sequence 59, Application PC/TUS0128124A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Biopanning and Rapid Analysis of Selective Interactive Ligands
; FILE REFERENCE: 005774.P004PCT
; CURRENT APPLICATION NUMBER: PCT/US01/28124A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(8)
; OTHER INFORMATION: synthetic construct
PCT-US01-28124A-59

Query Match          36.4%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
   |
Db 7 L 7

Search completed: December 13, 2001, 12:00:34
Job time: 297 sec
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 13, 2001, 11:55:37 ; Search time 174.34 Seconds  
(without alignments)  
12.741 Million cell updates/sec

Title: US-09-424-080A-1

Perfect score: 42

Sequence: -LTKKYSKP 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 36232

Minimum-DB-seq-length: 8

Maximum-DB-seq-length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /cgn2\_6/ptodata/2/paa/us099\_comb.pep.\*  
24: /cgn2\_6/ptodata/2/paa/us060\_comb.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	42	100.0	8	18	US-09-424-080-1
2	24	57.1	8	10	US-08-669-284-30
3	24	57.1	8	10	US-08-669-284A-30
4	24	57.1	8	11	US-08-704-499A-15
5	24	57.1	8	11	US-08-704-499A-16
6	24	57.1	8	16	US-09-232-186-15
7	24	57.1	8	16	US-09-232-186-16
8	21	50.0	8	3	US-07-722-489-409
9	21	50.0	8	8	US-08-403-590B-659

Sequence 659, Appl  
Sequence 29, Appl  
Sequence 30, Appl  
Sequence 31, Appl  
Sequence 32, Appl  
Sequence 2287, Ap  
Sequence 438, Ap  
Sequence 47, Appl  
Sequence 33, Appl  
Sequence 99, Appl  
Sequence 485, Appl  
Sequence 1615, Ap  
Sequence 3123, Ap  
Sequence 5295, Ap  
Sequence 7909, Ap  
Sequence 10223, A  
Sequence 10233, A  
Sequence 12092, A  
Sequence 47, Appl  
Sequence 33, Appl  
Sequence 11, Appl  
Sequence 73, Appl  
Sequence 73, Appl  
Sequence 48, Appl  
Sequence 65, Appl  
Sequence 65, Appl  
Sequence 48, Appl  
Sequence 1088, Ap  
Sequence 1089, Ap  
Sequence 1090, Ap  
Sequence 1091, Ap  
Sequence 4033, Ap  
Sequence 4034, Ap  
Sequence 7362, Ap  
Sequence 7367, Ap  
Sequence 65, Appl

## ALIGNMENTS

RESULT 1  
US-09-424-080-1  
; Sequence 1, Application US/09424080  
; GENERAL INFORMATION:  
; APPLICANT: ZAVIALOV, Vladimir et al.  
; TITLE OF INVENTION: COMPOSITION FOR ENHANCING IMMUNOSUPPRESSANTS PHARMACEUTICAL ACT  
; FILE REFERENCE: 0933-0149P  
; CURRENT APPLICATION NUMBER: US/09/424,080  
; CURRENT FILING DATE: 2000-02-14  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 1  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Immunosuppressants cycloporins, FK506, or rapamycin sequences  
; OTHER INFORMATION: derived from various organisms using sequence alignment.  
US-09-424-080-1

Query Match 100.0%; Score 42; DB 18; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.9e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTKKYSKP 8  
Db 1 LTKKYSKP 8

RESULT 2  
US-08-669-284-30

```

Sequence 30, Application US/08669284
GENERAL INFORMATION:
APPLICANT: Inoue, Makoto
APPLICANT: Kikuchi, Kaoru
APPLICANT: Ishige, Yoko
APPLICANT: Ito, Akira
APPLICANT: Kimura, Toru
APPLICANT: Nakayama, Chikao
APPLICANT: Noguchi, Hiroshi
TITLE OF INVENTION: NOVEL HUMAN CILIARY NEUTROPHILIC FACTORS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,284
FILING DATE: 28-JUN-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/02269
FILING DATE: 27-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 06-268281
FILING DATE: 05-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 06-201504
FILING DATE: 02-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-350934
FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: Q-42041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4..5
OTHER INFORMATION: /product= "See Table 3"
US-08-669-284-30

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Query Match 57.1%; Score 24; DB 10; Length 8;
Best Local Similarity 62.5%; Pred. No. 2.9e+06;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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```

QY 1 LTKKYSYSP 8
   |||||
DB 1 LTTXXYSYSP 8

```

```

RESULT 3
US-08-669-284A-30
; Sequence 30, Application US/08669284A
; GENERAL INFORMATION:

```

```

APPLICANT: Inoue, Makoto
APPLICANT: Kikuchi, Kaoru
APPLICANT: Ishige, Yoko
APPLICANT: Ito, Akira
APPLICANT: Kimura, Toru
APPLICANT: Nakayama, Chikao
APPLICANT: Noguchi, Hiroshi
TITLE OF INVENTION: NOVEL HUMAN CILIARY NEUTROPHILIC FACTORS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,284A
FILING DATE: 28-JUN-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/02269
FILING DATE: 27-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 06-268281
FILING DATE: 05-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 06-201504
FILING DATE: 02-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-350934
FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: Q-42041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4..5
OTHER INFORMATION: /product= "See Table 3"
US-08-669-284A-30

```

```

Query Match 57.1%; Score 24; DB 10; Length 8;
Best Local Similarity 62.5%; Pred. No. 2.9e+06;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 LTKKYSYSP 8
   |||||
DB 1 LTTXXYSYSP 8

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RESULT 4
US-08-704-499A-15
; Sequence 15, Application US/08704499A
; GENERAL INFORMATION:
APPLICANT: Rath, Matthias
; TITLE OF INVENTION: HYDROPHILIC SIGNAL

```

```

; TITLE OF INVENTION: OLIGOPEPTIDES AND METHODS OF THERAPEUTIC USE
; NUMBER OF SEQUENCES: 360
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INHOUSE IP MANAGEMENT
; STREET: 280 Colorado Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk, 3.50 inch, 1.44MB Storage
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: MS WORD 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,499A
; FILING DATE: AUGUST 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ALI KAMAREI
; REGISTRATION NUMBER: 37000
; REFERENCE/DOCKET NUMBER: 10262US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-7371
; TELEFAX: 415-322-7389
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-704-499A-15

Query Match 57.1%; Score 24; DB 11; Length 8;
Best Local Similarity 80.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TEKRY 6
Db 3 TEKRY 7

RESULT 5
US-08-704-499A-16
; Sequence 16, Application US/08704499A
; GENERAL INFORMATION:
; APPLICANT: Rath, Matthias
; TITLE OF INVENTION: HYDROPHILIC SIGNAL
; NUMBER OF SEQUENCES: 360
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INHOUSE IP MANAGEMENT
; STREET: 280 Colorado Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk, 3.50 inch, 1.44MB Storage
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: MS WORD 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,499A
; FILING DATE: AUGUST 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ALI KAMAREI
; REGISTRATION NUMBER: 37000
; REFERENCE/DOCKET NUMBER: 10262US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-7371

```

```

; TELEFAX: 415-322-7389
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-704-499A-16

Query Match 57.1%; Score 24; DB 11; Length 8;
Best Local Similarity 80.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TEKRY 6
Db 3 TEKRY 7

RESULT 6
US-09-232-186-15
; Sequence 15, Application US/09232186
; GENERAL INFORMATION:
; APPLICANT: Rath, Matthias
; TITLE OF INVENTION: METHOD OF PRODUCING VACCINES FROM PROTEIN SIGNAL OLIGOPEPTI
; NUMBER OF SEQUENCES: 360
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INHOUSE IP MANAGEMENT
; STREET: 280 Colorado Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk, 3.50 inch, 1.44MB Storage
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: MS WORD 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/232,186
; FILING DATE: JANUARY 13, 1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ALI KAMAREI
; REGISTRATION NUMBER: 37000
; REFERENCE/DOCKET NUMBER: 10262-1US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-322-7371
; TELEFAX: 650-322-7389
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-232-186-15

Query Match 57.1%; Score 24; DB 16; Length 8;
Best Local Similarity 80.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TEKRY 6
Db 3 TEKRY 7

RESULT 7
US-09-232-186-16
; Sequence 16, Application US/09232186
; GENERAL INFORMATION:
; APPLICANT: Rath, Matthias
; TITLE OF INVENTION: METHOD OF PRODUCING VACCINES FROM PROTEIN SIGNAL OLIGOPEPTI

```



NUMBER OF SEQUENCES: 360  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INHOUSE IP MANAGEMENT  
STREET: 280 Colorado Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk, 3.50 inch, 1.44MB Storage  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: WINDOWS 95  
SOFTWARE: MS WORD 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/232,186  
FILING DATE: JANUARY 13, 1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: ALI KAMAREI  
REGISTRATION NUMBER: 37000  
REFERENCE/DOCKET NUMBER: 10262-1US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-322-7371  
TELEFAX: 650-322-7389  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-232-186-16

Query Match 57.1%; Score 24; DB 16; Length 8;  
Best Local Similarity 80.0%; Pred. No. 2.9e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TEKRY 6  
DB 3 TEKRY 7

RESULT 8  
US-07-722-489-409  
Sequence 409, Application US/07722489  
GENERAL INFORMATION:  
APPLICANT: Chien, David Y.  
TITLE OF INVENTION: NANBV Diagnostics and Vaccines  
NUMBER OF SEQUENCES: 524  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/722.489  
FILING DATE: 19910624  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Blackburn, Robert P.  
REGISTRATION NUMBER: 30,447  
REFERENCE/DOCKET NUMBER: 0110.031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2702  
TELEFAX: (510) 655-3542(2)

INFORMATION FOR SEQ ID NO: 409:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-722-489-409

Query Match 50.0%; Score 21; DB 3; Length 8;  
Best Local Similarity 66.7%; Pred. No. 2.9e+06;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERKY 6  
DB 1 LTERLY 6

RESULT 9  
US-08-403-590B-659  
Sequence 659, Application US/08403590B  
GENERAL INFORMATION:  
APPLICANT: Chien, David Y.  
TITLE OF INVENTION: NANBV Diagnostics and Vaccines  
NUMBER OF SEQUENCES: 777  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,590B  
FILING DATE: 14-MAR-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Harbin, Ailsa A.  
REGISTRATION NUMBER: 33,895  
REFERENCE/DOCKET NUMBER: 0110.002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (508)359-3876  
TELEFAX: (508)359-3885

INFORMATION FOR SEQ ID NO: 659:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-403-590B-659

Query Match 50.0%; Score 21; DB 8; Length 8;  
Best Local Similarity 66.7%; Pred. No. 2.9e+06;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERKY 6  
DB 1 LTERLY 6

RESULT 10  
US-08-444-112-659  
Sequence 659, Application US/08444112  
GENERAL INFORMATION:

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; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANB Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,112
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hardin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110,002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 659:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-444-112-659

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```

Query Match 50.0%; Score 21; DB 8; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.9e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 LFEKKY 6
Db 1 LTERLY 6

```

```

RESULT 11
US-09-535-529-29
; Sequence 29, Application US/09535529
; GENERAL INFORMATION:
; APPLICANT: JUNGBAUER, ALOIS
; APPLICANT: JOSIC, DJURO
; APPLICANT: NECINA, ROMAN
; TITLE OF INVENTION: PEPTIDE HAVING AFFINITY FOR COAGULATION FACTOR-VIII
; FILE REFERENCE: 10496/P65152US0
; CURRENT APPLICATION NUMBER: US/09/535,529
; CURRENT FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 29
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-535-529-29

```

```

Query Match 50.0%; Score 21; DB 19; Length 8;

```

```

Best Local Similarity 60.0%; Pred. No. 2.9e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 4 KKYP 8
Db 4 KEYP 8

```

```

RESULT 12
US-09-535-529-30
; Sequence 30, Application US/09535529
; GENERAL INFORMATION:
; APPLICANT: JUNGBAUER, ALOIS
; APPLICANT: JOSIC, DJURO
; APPLICANT: NECINA, ROMAN
; TITLE OF INVENTION: PEPTIDE HAVING AFFINITY FOR COAGULATION FACTOR VIII
; FILE REFERENCE: 10496/P65152US0
; CURRENT APPLICATION NUMBER: US/09/535,529
; CURRENT FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 30
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; US-09-535-529-30

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Query Match 50.0%; Score 21; DB 19; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.9e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 4 KKYP 8
Db 3 KEYP 7

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```

RESULT 13
US-09-535-529-31
; Sequence 31, Application US/09535529
; GENERAL INFORMATION:
; APPLICANT: JUNGBAUER, ALOIS
; APPLICANT: JOSIC, DJURO
; APPLICANT: NECINA, ROMAN
; TITLE OF INVENTION: PEPTIDE HAVING AFFINITY FOR COAGULATION FACTOR VIII
; FILE REFERENCE: 10496/P65152US0
; CURRENT APPLICATION NUMBER: US/09/535,529
; CURRENT FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 31
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; US-09-535-529-31

```

```

Query Match 50.0%; Score 21; DB 19; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.9e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 4 KKYP 8
Db 2 KEYP 6

```

```

RESULT 14

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Thu Dec 13 12:06:08 2001

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US-09-535-529-32
; Sequence 32, Application US/09535529
; GENERAL INFORMATION:
; APPLICANT: JUNGRAUER, ALOIS
; APPLICANT: JOSIC, DURO
; APPLICANT: NECINA, ROMAN
; TITLE OF INVENTION: PEPTIDE HAVING AFFINITY FOR COAGULATION FACTOR VIII
; FILE REFERENCE: 10496/P65152US0
; CURRENT APPLICATION NUMBER: US/09/535,529
; CURRENT FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-535-529-32

Query Match          50.0%; Score 21; DB 19; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.9e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKYP 8
Db 1 KEYP 5

RESULT 15
US-09-633-364-2287
; Sequence 2287, Application US/09633364
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Eteban
; APPLICANT: Keogh, Elissa
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: Prostate Cancer Antigens Using Peptide and Nucleic Acid
; FILE REFERENCE: 018623-014710US
; CURRENT APPLICATION NUMBER: US/09/633,364
; CURRENT FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/171,312
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 6899
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2287
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-633-364-2287

Query Match          50.0%; Score 21; DB 20; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.9e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKKYP 8
Db 1 EKYP 6
```

Search completed: December 13, 2001, 12:00:19  
Job time: 282 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 13, 2001, 11:55:37 ; Search time 9.12 Seconds  
(without alignments)  
10.106 Million cell updates/sec

Title: US-09-424-080A-1

Perfect score: 42  
Sequence: LITEKKYSP 8

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 61579 seqs, 11521160 residues

Total number of hits satisfying chosen parameters: 876

Minimum DB seq length: 8  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_Nov.\*

- 1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pap.\*
- 2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pap.\*
- 3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pap.\*
- 4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pap.\*
- 5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pap.\*
- 6: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	42	100.0	8	5	US-09-424-080A-1
2	18	42.9	8	5	US-09-620-394B-8370
3	18	42.9	8	5	US-09-637-780B-640
4	18	42.9	8	5	US-09-849-092A-2
5	17	40.5	8	5	US-09-104-337A-466
6	17	40.5	8	5	US-09-528-200-38
7	17	40.5	8	5	US-09-528-200-44
8	17	40.5	8	5	US-09-528-200-50
9	16	38.1	8	5	US-09-104-337A-423
10	16	38.1	8	5	US-09-763-982-12
11	16	38.1	8	5	US-09-620-394B-8589
12	16	38.1	8	5	US-09-485-345-10
13	16	38.1	8	5	US-09-637-780B-859
14	15	35.7	8	1	PCT-US01-28124A-134
15	15	35.7	8	5	US-09-622-978-18
16	15	35.7	8	5	US-09-104-337A-478
17	15	35.7	8	5	US-09-104-337A-526
18	15	35.7	8	5	US-09-486-625A-24
19	15	35.7	8	5	US-09-938-497-6
20	15	35.7	8	5	US-09-423-468A-9
21	15	35.7	8	5	US-09-897-107-39
22	15	35.7	8	5	US-09-897-107-43
23	14	33.3	8	5	US-09-973-278-661
24	14	33.3	8	5	US-09-104-337A-363
25	14	33.3	8	5	US-09-104-337A-448
26	14	33.3	8	5	US-09-104-337A-496
27	14	33.3	8	5	US-09-104-337A-504

28	14	33.3	8	5	US-09-295-996A-14	Sequence 14, Appl
29	14	33.3	8	5	US-09-982-172-123	Sequence 123, App
30	14	33.3	8	5	US-09-763-982-8	Sequence 8, Appl
31	14	33.3	8	5	US-09-831-047C-121	Sequence 121, App
32	14	33.3	8	5	US-09-837-138-22	Sequence 22, Appl
33	13	31.0	8	4	US-08-816-454B-114	Sequence 114, App
34	13	31.0	8	5	US-09-966-707-20	Sequence 20, Appl
35	13	31.0	8	5	US-09-856-812-14	Sequence 14, Appl
36	13	31.0	8	5	US-09-852-424-52	Sequence 52, Appl
37	13	31.0	8	5	US-09-705-160-40	Sequence 40, Appl
38	13	31.0	8	5	US-09-524-782-18	Sequence 18, Appl
39	13	31.0	8	5	US-09-620-394B-8419	Sequence 8419, Ap
40	13	31.0	8	5	US-09-574-735C-34	Sequence 34, Appl
41	13	31.0	8	5	US-09-637-780B-689	Sequence 689, App
42	13	31.0	8	5	US-09-169-717E-13	Sequence 13, Appl
43	13	31.0	8	5	US-09-938-406-16	Sequence 16, Appl
44	12	28.6	8	1	PCT-US01-28124A-52	Sequence 52, Appl
45	12	28.6	8	4	US-08-816-454B-173	Sequence 173, App

## ALIGNMENTS

RESULT 1  
US-09-424-080A-1  
; Sequence 1, Application US/09424080A  
; GENERAL INFORMATION: Vladimir et al.  
; APPLICANT: ZAVIALOV, Vladimir et al.  
; TITLE OF INVENTION: COMPOSITION FOR ENHANCING IMMUNOSUPPRESSANTS PHARMACEUTICAL ACT  
; FILE REFERENCE: 0933-0149P  
; CURRENT APPLICATION NUMBER: US/09/424,080A  
; CURRENT FILING DATE: 2000-02-14  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: A peptide corresponding to the high-affinity binding/anti-lymphoproliferative  
; OTHER INFORMATION: site of human IFN-alpha  
US-09-424-080A-1

Query Match 100.0%; Score 42; DB 5; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.4e+04;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LITEKKYSP 8  
Db 1 LITEKKYSP 8

RESULT 2  
US-09-620-394B-8370  
; Sequence 8370, Application US/09620394B  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai  
; APPLICANT: BROVER, Vyacheslav  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid  
; TITLE OF INVENTION: Thereby  
; FILE REFERENCE: 2750-1067P  
; CURRENT APPLICATION NUMBER: US/09/620,394B  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 9131  
; SEQ ID NO 8370  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus Pattern from various organisms  
US-09-620-394B-8370

Query Match 42.9%; Score 18; DB 5; Length 8;  
Best Local Similarity 60.0%; Pred. No. 5.4e+04;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 EKKYS 7  
DB 2 EKRHS 6

RESULT 3  
US-09-637-780B-640  
; Sequence 640, Application US/09637780B  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai  
; APPLICANT: BROVER, Vyacheslav  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: Thereby  
; CURRENT FILING DATE: 2750-1096P  
; CURRENT APPLICATION NUMBER: US/09/637,780B  
; NUMBER OF SEQ ID NOS: 2000-08-11  
; SEQ ID NO 640  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus Pattern from various organisms  
US-09-637-780B-640

Query Match 42.9%; Score 18; DB 5; Length 8;  
Best Local Similarity 60.0%; Pred. No. 5.4e+04;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 EKKYS 7  
DB 2 EKRHS 6

RESULT 4  
US-09-849-092A-2  
; Sequence 2, Application US/09849092A  
; GENERAL INFORMATION:  
; APPLICANT: Eriksson, Ulf; Simon, Andras; Romert, Anna  
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE WHICH  
; CODES FOR A 32 KDA PROTEIN HAVING 11-CIS RETINOL DEHYDROGEN  
; ACTIVITY, AND WHICH ASSOCIATES WITH P63, A PORTION OF A  
; RETINOL BINDING PROTEIN RECEPTOR  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York City  
; STATE: New York  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage  
; COMPUTER: IBM  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/849,092A  
; FILING DATE: 04-May-2001  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/729,594  
; FILING DATE: 1998-01-27  
; APPLICATION NUMBER: 08/375,962  
; FILING DATE: 20-January-1995  
; APPLICATION NUMBER: 08/258,418  
; FILING DATE: 10-June-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, Norman D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5372.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-849-092A-2

Query Match 42.9%; Score 18; DB 5; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.4e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YSP 8  
DB 1 YSP 3

RESULT 5  
US-09-104-337A-466  
; Sequence 466, Application US/09104337A  
; GENERAL INFORMATION:  
; APPLICANT: Winter, Gregory Paul  
; Griffiths, Andrew David  
; Williams, Samuel Cameron  
; Waterhouse, Peter  
; Nissim, Ahuva  
; Johnson, Kevin Stuart  
; Smith, Andrew John Hammond  
; TITLE OF INVENTION: Methods for producing members of specific  
; binding pairs  
; NUMBER OF SEQUENCES: 600  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Audrey L. Bartnicki  
; STREET: Marshall, Gerstein & Borun  
; 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA: US/09/104,337A  
; APPLICATION NUMBER: US/09/104,337A  
; FILING DATE: 25-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/350,260  
; FILING DATE: 05-DEC-1994  
; APPLICATION NUMBER: GB 9110549.4  
; FILING DATE: 15-MAY-1991  
; APPLICATION NUMBER: GB 9206318.9  
; FILING DATE: 24-MAR-1992  
; APPLICATION NUMBER: PCT/GB92/00883  
; FILING DATE: 15-MAY-1992  
; APPLICATION NUMBER: PCT/GB93/00605  
; FILING DATE: 24-MAR-1993  
; APPLICATION NUMBER: US 08/150,002  
; FILING DATE: 31-MAR-1994  
; APPLICATION NUMBER: US 08/307,619  
; FILING DATE: 16-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
NAME: Bartnicki, Audrey L.

REGISTRATION NUMBER: 40,499  
 REFERENCE/DOCKET NUMBER: 28111/32372A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312-474-6300  
 INFORMATION FOR SEQ ID NO: 466:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 466:  
 US-09-104-337A-466

Query Match 40.5%; Score 17; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 4 KKY 6  
 |||  
 Db 1 KKY 3

RESULT 6  
 US-09-528-200-38  
 ; Sequence 38, Application US/09528200  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LICHIA, KAI  
 ; APPLICANT: BECKER, ANDREAS  
 ; APPLICANT: SEMMLER, WOLFHARD  
 ; APPLICANT: WEIDENMANN, BERTRAM  
 ; APPLICANT: HESSNIUS, CARSTEN  
 ; APPLICANT: VOLKMER-ENGERT, RUDOLF  
 ; APPLICANT: SCHNEIDER-MERGNER, JENS  
 ; APPLICANT: BHARGAVA, SARAH  
 ; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA  
 ; FILE OF INVENTION: FOR OPTICAL DIAGNOSIS  
 ; FILE REFERENCE: SCH-1731  
 ; CURRENT APPLICATION NUMBER: US/09/528,200  
 ; CURRENT FILING DATE: 2000-03-17  
 ; PRIOR APPLICATION NUMBER: DE 199 17 713.9  
 ; PRIOR FILING DATE: 1999-09-04  
 ; NUMBER OF SEQ ID NOS: 196  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 38  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-528-200-38

Query Match 40.5%; Score 17; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 4 KKY 6  
 |||  
 Db 3 KKY 5

RESULT 7  
 US-09-528-200-44  
 ; Sequence 44, Application US/09528200  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LICHIA, KAI  
 ; APPLICANT: BECKER, ANDREAS  
 ; APPLICANT: SEMMLER, WOLFHARD  
 ; APPLICANT: WEIDENMANN, BERTRAM  
 ; APPLICANT: HESSNIUS, CARSTEN  
 ; APPLICANT: VOLKMER-ENGERT, RUDOLF  
 ; APPLICANT: SCHNEIDER-MERGNER, JENS  
 ; APPLICANT: BHARGAVA, SARAH  
 ; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA

; TITLE OF INVENTION: FOR OPTICAL DIAGNOSIS  
 ; FILE REFERENCE: SCH-1731  
 ; CURRENT APPLICATION NUMBER: US/09/528,200  
 ; CURRENT FILING DATE: 2000-03-17  
 ; PRIOR APPLICATION NUMBER: DE 199 17 713.9  
 ; PRIOR FILING DATE: 1999-09-04  
 ; NUMBER OF SEQ ID NOS: 196  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 44  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-528-200-44

Query Match 40.5%; Score 17; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 4 KKY 6  
 |||  
 Db 4 KKY 6

RESULT 8  
 US-09-528-200-50  
 ; Sequence 50, Application US/09528200  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LICHIA, KAI  
 ; APPLICANT: BECKER, ANDREAS  
 ; APPLICANT: SEMMLER, WOLFHARD  
 ; APPLICANT: WEIDENMANN, BERTRAM  
 ; APPLICANT: HESSNIUS, CARSTEN  
 ; APPLICANT: VOLKMER-ENGERT, RUDOLF  
 ; APPLICANT: SCHNEIDER-MERGNER, JENS  
 ; APPLICANT: BHARGAVA, SARAH  
 ; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA  
 ; FILE OF INVENTION: FOR OPTICAL DIAGNOSIS  
 ; FILE REFERENCE: SCH-1731  
 ; CURRENT APPLICATION NUMBER: US/09/528,200  
 ; CURRENT FILING DATE: 2000-03-17  
 ; PRIOR APPLICATION NUMBER: DE 199 17 713.9  
 ; PRIOR FILING DATE: 1999-09-04  
 ; NUMBER OF SEQ ID NOS: 196  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 50  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-528-200-50

Query Match 40.5%; Score 17; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 4 KKY 6  
 |||  
 Db 5 KKY 7

RESULT 9  
 US-09-104-337A-423  
 ; Sequence 423, Application US/09104337A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Winter, Gregory Paul  
 ; Griffiths, Andrew David  
 ; Williams, Samuel Cameron  
 ; Waterhouse, Peter  
 ; Nissim, Ahuva  
 ; Johnson, Kevin Stuart  
 ; Smith, Andrew John Hammond  
 ; TITLE OF INVENTION: Methods for producing members of specific

binding pairs  
NUMBER OF SEQUENCES: 600  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Audrey L. Bartnicki  
STREET: Marshall, Gerstein & Borun  
6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA: US/09/104,337A  
FILING DATE: 25-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/350,260  
FILING DATE: 03-DEC-1994  
APPLICATION NUMBER: GB 9110549.4  
FILING DATE: 15-MAY-1991  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
APPLICATION NUMBER: PCT/GB92/00883  
FILING DATE: 15-MAY-1992  
APPLICATION NUMBER: PCT/GB93/00605  
FILING DATE: 24-MAR-1993  
APPLICATION NUMBER: US 08/150,002  
FILING DATE: 31-MAR-1994  
APPLICATION NUMBER: US 08/307,619  
FILING DATE: 16-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bartnicki, Audrey L.  
REGISTRATION NUMBER: 40,499  
REFERENCE/DOCKET NUMBER: 28111/32372A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
INFORMATION FOR SEQ ID NO: 423:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 423:  
US-09-104-337A-423

Query Match 38.1%; Score 16; DB 5; Length 8;  
Best Local Similarity 50.0%; Pred. No. 5.4e+04;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 3 EKKY 6  
DB 2 ORKY 5  
RESULT 10  
US-09-763-982-12  
; Sequence 12, Application US/09763982  
; GENERAL INFORMATION:  
; APPLICANT: Diamond, Scott L  
; TITLE OF INVENTION: THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA  
; TITLE OF INVENTION: PEPTIDE SCAFFOLDS FOR TRANSFER OF MOLECULES INTO  
; FILE REFERENCE: PENN-0698  
; CURRENT APPLICATION NUMBER: US/09/763,982  
; PRIOR FILING DATE: 2001-09-21  
; PRIOR APPLICATION NUMBER: 60/098,791  
; PRIOR FILING DATE: 1998-09-01  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 12  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-763-982-12

Query Match 38.1%; Score 16; DB 5; Length 8;  
Best Local Similarity 75.0%; Pred. No. 5.4e+04;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TEKK 5  
DB 3 TKKK 6

RESULT 11  
US-09-620-394B-8589  
; Sequence 8589, Application US/09620394B  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai  
; APPLICANT: BROVER, Vyacheslav  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid  
; FILE REFERENCE: 2750-1067P  
; CURRENT APPLICATION NUMBER: US/09/620,394B  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 9131  
; SEQ ID NO 8589  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus Pattern from various organisms  
US-09-620-394B-8589

Query Match 38.1%; Score 16; DB 5; Length 8;  
Best Local Similarity 75.0%; Pred. No. 5.4e+04;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TEKK 5  
DB 3 TEKK 6

RESULT 12  
US-09-485-345-10  
; Sequence 10, Application US/09485345  
; GENERAL INFORMATION:  
; APPLICANT: Acres, Bruce  
; TITLE OF INVENTION: TGF-beta RII Receptor Nucleic Sequence, Coded Peptide, and Uses  
; FILE REFERENCE: 032847-003  
; CURRENT APPLICATION NUMBER: US/09/485,345  
; CURRENT FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: PCT/FR99/01354  
; PRIOR FILING DATE: 1999-06-08  
; PRIOR APPLICATION NUMBER: FR 98/07322  
; PRIOR FILING DATE: 1998-06-08  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide capable of binding to at least one MHC I  
US-09-485-345-10

Query Match 38.1%; Score 16; DB 5; Length 8;  
Best Local Similarity 60.0%; Pred. No. 5.4e+04;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTKK 5  
DB 2 MKEKK 6

## RESULT 13

US-09-637-780B-859  
; Sequence 859, Application US/09637780B  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai  
; APPLICANT: BROVER, Vyacheslav  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1096P  
; CURRENT APPLICATION NUMBER: US/09/637,780B  
; CURRENT FILING DATE: 2000-08-11  
; NUMBER OF SEQ ID NOS: 1401  
; SEQ ID NO 859  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus Pattern from various organisms  
US-09-637-780B-859

Query Match 38.1%; Score 16; DB 5; Length 8;  
Best Local Similarity 75.0%; Pred. No. 5.4e+04;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TEKK 5  
DB 3 TEQK 6

## RESULT 14

PCT-US01-28124A-134  
; Sequence 134, Application PC/TUS0128124A  
; GENERAL INFORMATION:  
; APPLICANT: Board of Regents, The University of Texas System  
; TITLE OF INVENTION: Biopanning and Rapid Analysis of Selective Interactive Ligands (B  
; FILE REFERENCE: 005774.P004PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/28124A  
; CURRENT FILING DATE: 2001-09-07  
; NUMBER OF SEQ ID NOS: 289  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 134  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: (1)..(8)  
; OTHER INFORMATION: synthetic construct  
PCT-US01-28124A-134

Query Match 35.7%; Score 15; DB 1; Length 8;  
Best Local Similarity 66.7%; Pred. No. 5.4e+04;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 YSP 8  
DB 4 YNP 6

## RESULT 15

US-09-622-978-18  
; Sequence 18, Application US/09622978

; GENERAL INFORMATION:  
; APPLICANT: Hull, Roger  
; APPLICANT: Harper, Glyn  
; TITLE OF INVENTION: Banana streak virus promoter and detection  
; FILE REFERENCE: 620-106  
; CURRENT APPLICATION NUMBER: US/09/622,978  
; CURRENT FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: PCT/GB99/00599  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: GB 9804293.0  
; PRIOR FILING DATE: 1998-02-27  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Musa acuminata  
; OTHER INFORMATION: US-09-622-978-18

Query Match 35.7%; Score 15; DB 5; Length 8;  
Best Local Similarity 66.7%; Pred. No. 5.4e+04;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 YSP 8  
DB 4 YNP 6

Search completed: December 13, 2001, 12:00:34  
Job time: 297 sec





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Thu Dec 13 10:55:19 2001

```

QY      1 L 1
Db      1 L 1

RESULT 2
PCT-US00-29363-207
; Sequence 207, Application PC/TUS0029363
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 22 Human Secreted Proteins
; FILE REFERENCE: PS701PCT
; CURRENT APPLICATION NUMBER: PCT/US00/29363
; CURRENT FILING DATE: 2000-10-25
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/215,139
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 207
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-29363-207

Query Match      36.4%; Score 4; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 L 1
Db      1 L 1

RESULT 3
PCT-US00-30040A-163
; Sequence 163, Application PC/TUS0030040A
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 24 Human Secreted Proteins
; FILE REFERENCE: PS706PCT
; CURRENT APPLICATION NUMBER: PCT/US00/30040A
; CURRENT FILING DATE: 2000-11-01
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/163,580
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 163
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-30040A-163

Query Match      36.4%; Score 4; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 L 1
Db      1 L 1

RESULT 4
PCT-US00-30040A-172
; Sequence 172, Application PC/TUS0030040A
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 24 Human Secreted Proteins
; FILE REFERENCE: PS714PCT
; CURRENT APPLICATION NUMBER: PCT/US00/30629
; CURRENT FILING DATE: 2000-11-08
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/164,825
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 109
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-30040A-172

Query Match      36.4%; Score 4; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 L 1
Db      1 L 1

RESULT 5
PCT-US00-30045-154
; Sequence 154, Application PC/TUS0030045
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PS708PCT
; CURRENT APPLICATION NUMBER: PCT/US00/30045
; CURRENT FILING DATE: 2000-11-01
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/163,581
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 201
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 154
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-30045-154

Query Match      36.4%; Score 4; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 L 1
Db      1 L 1

RESULT 6
PCT-US00-30629-109
; Sequence 109, Application PC/TUS0030629
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 24 Human Secreted Proteins
; FILE REFERENCE: PS714PCT
; CURRENT APPLICATION NUMBER: PCT/US00/30629
; CURRENT FILING DATE: 2000-11-08
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/164,825
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 109
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-30629-109

Query Match      36.4%; Score 4; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 L 1
Db      1 L 1

```

;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
PCT-US00-30629-109

Query Match 36.4%; Score 4; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
|  
Db 1 L 1

RESULT 7  
PCT-US00-30629-160  
;; Sequence 160, Application PC/TUS0030629  
;; GENERAL INFORMATION:  
;; APPLICANT: Human Genome Sciences, Inc.  
;; TITLE OF INVENTION: 24 Human Secreted Proteins  
;; FILE REFERENCE: PS714PCT  
;; CURRENT FILING DATE: 2000-11-08  
;; PRIOR APPLICATION NUMBER: PCT/US00/30629  
;; PRIOR FILING DATE: 1999-11-12  
;; PRIOR APPLICATION NUMBER: 60/164,825  
;; PRIOR FILING DATE: 1999-11-12  
;; PRIOR APPLICATION NUMBER: 60/222,904  
;; PRIOR FILING DATE: 2000-08-03  
;; NUMBER OF SEQ ID NOS: 189  
;; SOFTWARE: Patentin Ver. 2.0  
;; SEQ ID NO 160  
;; LENGTH: 2  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
PCT-US00-30629-160

Query Match 36.4%; Score 4; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
|  
Db 1 L 1

RESULT 8  
PCT-US00-30653-208  
;; Sequence 208, Application PC/TUS0030653  
;; GENERAL INFORMATION:  
;; APPLICANT: Human Genome Sciences, Inc.  
;; TITLE OF INVENTION: 35 Human Secreted Proteins  
;; FILE REFERENCE: PS713PCT  
;; CURRENT FILING DATE: 2000-11-08  
;; PRIOR APPLICATION NUMBER: PCT/US00/30653  
;; PRIOR FILING DATE: 2000-11-08  
;; PRIOR APPLICATION NUMBER: 60/164,735  
;; PRIOR FILING DATE: 1999-11-12  
;; PRIOR APPLICATION NUMBER: 60/221,193  
;; PRIOR FILING DATE: 2000-07-27  
;; NUMBER OF SEQ ID NOS: 289  
;; SOFTWARE: Patentin Ver. 2.0  
;; SEQ ID NO 208  
;; LENGTH: 2  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
PCT-US00-30653-208

Query Match 36.4%; Score 4; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
|

Db 2 L 2

RESULT 9  
PCT-US01-01786A-159  
;; Sequence 159, Application PC/TUS0101786A  
;; GENERAL INFORMATION:  
;; APPLICANT: SMITHKLINE BEECHAM CORPORATION  
;; APPLICANT: SMITHKLINE BEECHAM P.L.C.  
;; TITLE OF INVENTION: METHODS AND REAGENTS FOR PERFORMING  
;; TITLE OF INVENTION: ANTIMICROBIAL COMPOUND SCREENING  
;; FILE REFERENCE: GMS0067  
;; CURRENT APPLICATION NUMBER: PCT/US01/01786A  
;; CURRENT FILING DATE: 2001-01-17  
;; PRIOR APPLICATION NUMBER: 60/176,870  
;; PRIOR FILING DATE: 2000-01-18  
;; NUMBER OF SEQ ID NOS: 403  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 159  
;; LENGTH: 2  
;; TYPE: PRT  
;; ORGANISM: Escherichia coli  
PCT-US01-01786A-159

Query Match 36.4%; Score 4; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
|  
Db 1 L 1

RESULT 10  
PCT-US01-11988-168  
;; Sequence 168, Application PC/TUS0111988  
;; GENERAL INFORMATION:  
;; APPLICANT: Human Genome Sciences, Inc.  
;; TITLE OF INVENTION: Albumin Fusion Proteins  
;; FILE REFERENCE: PF546PCT  
;; CURRENT APPLICATION NUMBER: PCT/US01/11988  
;; CURRENT FILING DATE: 2001-01-12  
;; PRIOR APPLICATION NUMBER: 60/229,358  
;; PRIOR FILING DATE: 2000-04-12  
;; PRIOR APPLICATION NUMBER: 60/256,931  
;; PRIOR FILING DATE: 2000-12-21  
;; PRIOR APPLICATION NUMBER: 60/199,384  
;; PRIOR FILING DATE: 2000-04-25  
;; NUMBER OF SEQ ID NOS: 2267  
;; SOFTWARE: Patentin Ver. 2.1  
;; SEQ ID NO 168  
;; LENGTH: 2  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
PCT-US01-11988-168

Query Match 36.4%; Score 4; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
|  
Db 1 L 1

RESULT 11  
PCT-US01-11988-476  
;; Sequence 476, Application PC/TUS0111988  
;; GENERAL INFORMATION:  
;; APPLICANT: Human Genome Sciences, Inc.  
;; TITLE OF INVENTION: Albumin Fusion Proteins

```

; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: PCT/US01/11988
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 476
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-11988-476

```

```

Query Match          36.4%; Score 4; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 L 1
Db 1 L 1

```

```

RESULT 12
PCT-US01-11988-494
; Sequence 494, Application PC/TUS0111988
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: PCT/US01/11988
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 494
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-11988-494

```

```

Query Match          36.4%; Score 4; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 L 1
Db 2 L 2

```

```

RESULT 13
PCT-US01-11988-665
; Sequence 665, Application PC/TUS0111988
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: PCT/US01/11988
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21

```

```

; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 665
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-11988-665

```

```

Query Match          36.4%; Score 4; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 L 1
Db 1 L 1

```

```

RESULT 14
PCT-US01-11988-1055
; Sequence 1055, Application PC/TUS0111988
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: PCT/US01/11988
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1055
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-11988-1055

```

```

Query Match          36.4%; Score 4; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 L 1
Db 2 L 2

```

```

RESULT 15
PCT-US01-11988-1071
; Sequence 1071, Application PC/TUS0111988
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: PCT/US01/11988
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1071
; LENGTH: 2
; TYPE: PRT

```

us-09-424-080a-2.open.rapm

Thu Dec 13 10:55:19 2001

ORGANISM: Homo sapiens  
PCT-US01-11988-1071

Query Match 36.4%; Score 4; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
|  
Db 1 L 1

Search completed: December 13, 2001, 10:49:32  
Job time: 292 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 13, 2001, 10:49:47 ; Search time 9.21 Seconds  
(without alignments)  
10.008 Million cell updates/sec

Title: US-09-424-080A-2

Perfect score: 11

Sequence: 1 LXXXXXX 8

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 61579 seqs, 11521160 residues

Total number of hits satisfying chosen parameters: 61579

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents\_AA\_New:\*

- 1: /cgn2\_6/ptodata/1/paa/pct\_NEW\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	2	5	US-09-982-172-96
2	4	36.4	2	5	US-09-982-172-153
3	4	36.4	2	5	US-09-720-934-101
4	4	36.4	3	1	PCT-US01-27692A-138
5	4	36.4	3	1	PCT-US01-27692A-142
6	4	36.4	3	1	PCT-US01-27692A-161
7	4	36.4	3	1	PCT-US01-27692A-179
8	4	36.4	3	1	PCT-US01-27692A-181
9	4	36.4	3	1	PCT-US01-28044A-8
10	4	36.4	3	1	PCT-US01-28044A-9
11	4	36.4	3	1	PCT-US01-28044A-10
12	4	36.4	3	1	PCT-US01-28044A-15
13	4	36.4	3	1	PCT-US01-28044A-21
14	4	36.4	3	1	PCT-US01-28044A-130
15	4	36.4	3	1	PCT-US01-28044A-306
16	4	36.4	3	1	PCT-US01-28044A-307
17	4	36.4	3	1	PCT-US01-28044A-309
18	4	36.4	3	1	PCT-US01-28044A-314
19	4	36.4	3	1	PCT-US01-28044A-323
20	4	36.4	3	1	PCT-US01-28044A-345
21	4	36.4	3	1	PCT-US01-28044A-355
22	4	36.4	3	1	PCT-US01-28044A-361
23	4	36.4	3	1	PCT-US01-28044A-363
24	4	36.4	3	1	PCT-US01-28044A-367
25	4	36.4	3	1	PCT-US01-28044A-377
26	4	36.4	3	1	PCT-US01-28044A-380
27	4	36.4	3	1	PCT-US01-28044A-397

28	4	36.4	3	1	PCT-US01-28044A-405	Sequence 405, App
29	4	36.4	3	1	PCT-US01-28044A-406	Sequence 406, App
30	4	36.4	3	1	PCT-US01-28044A-407	Sequence 407, App
31	4	36.4	3	1	PCT-US01-28044A-408	Sequence 408, App
32	4	36.4	3	1	PCT-US01-28044A-409	Sequence 409, App
33	4	36.4	3	1	PCT-US01-28044A-418	Sequence 418, App
34	4	36.4	3	1	PCT-US01-28044A-421	Sequence 421, App
35	4	36.4	3	1	PCT-US01-28044A-423	Sequence 423, App
36	4	36.4	3	5	US-09-967-772-12	Sequence 12, App
37	4	36.4	3	5	US-09-982-172-48	Sequence 48, App
38	4	36.4	3	5	US-09-982-172-54	Sequence 54, App
39	4	36.4	3	5	US-09-720-934-33	Sequence 33, App
40	4	36.4	3	5	US-09-720-934-65	Sequence 65, App
41	4	36.4	3	5	US-09-720-934-99	Sequence 99, App
42	4	36.4	3	5	US-09-922-261-7	Sequence 7, App
43	4	36.4	3	5	US-09-922-261-310	Sequence 310, App
44	4	36.4	3	5	US-09-922-261-385	Sequence 385, App
45	4	36.4	4	5	US-09-721-477-71	Sequence 71, App

## ALIGNMENTS

## RESULT 1

US-09-982-172-96  
Sequence 96, Application US/09982172

GENERAL INFORMATION:

APPLICANT: Emil Israel Katz

TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODY  
DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENE  
UTILIZING EACH

FILE REFERENCE: 01/22283

CURRENT APPLICATION NUMBER: US/09/982,172

CURRENT FILING DATE: 2001-10-19

NUMBER OF SEQ ID NOS: 253

SOFTWARE: PatentIn version 3.1

SEQ ID NO 96

LENGTH: 2

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: Computer generated synthetic peptide

US-09-982-172-96

Query Match 36.4%; Score 4; DB 5; Length 2;  
Best Local Similarity 100.0%; Pred. No. 4.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1

Db 1 L 1

## RESULT 2

US-09-982-172-153

Sequence 153, Application US/09982172

GENERAL INFORMATION:

APPLICANT: Emil Israel Katz

TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODY  
DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENE  
UTILIZING EACH

FILE REFERENCE: 01/22283

CURRENT APPLICATION NUMBER: US/09/982,172

CURRENT FILING DATE: 2001-10-19

NUMBER OF SEQ ID NOS: 253

SOFTWARE: PatentIn version 3.1

SEQ ID NO 153

LENGTH: 2

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: Computer generated synthetic peptide

US-09-982-172-153

Thu Dec 13 10:55:20 2001

US-09-982-172-153		PCT-US01-27692A-142	
Query Match		Sequence 142, Application PC/TUS0127692A	
Best Local Similarity		APPLICANT: Board of Regents, The University of Texas System	
Matches	1; Conservative	TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display	
	0; Mismatches	FILE REFERENCE: 005774.P003PCT	
	0; Indels	CURRENT APPLICATION NUMBER: PCT/US01/27692A	
	0; Gaps	CURRENT FILING DATE: 2001-09-07	
	0; Indels	NUMBER OF SEQ ID NOS: 251	
	0; Gaps	SOFTWARE: PatentIn version 3.1	
	0; Indels	SEQ ID NO 142	
	0; Gaps	LENGTH: 3	
	0; Indels	TYPE: PRT	
	0; Gaps	ORGANISM: Artificial Sequence	
	0; Indels	NAME/KEY: Peptide	
	0; Gaps	LOCATION: (1)..(3)	
	0; Indels	OTHER INFORMATION: synthetic construct	
	0; Gaps	PCT-US01-27692A-142	
	0; Indels	Query Match	
	0; Gaps	Best Local Similarity	
	0; Indels	Matches	
	0; Gaps	Score 4; DB 1; Length 3;	
	0; Indels	Pred. No. 4.8e+04;	
	0; Gaps	Mismatches 0; Indels 0; Gaps 0;	
	0; Indels	OY	
	0; Gaps	L L 1	
	0; Indels	Db	
	0; Gaps	1 L 1	
	0; Indels	RESULT 6	
	0; Gaps	PCT-US01-27692A-161	
	0; Indels	Sequence 161, Application PC/TUS0127692A	
	0; Gaps	GENERAL INFORMATION:	
	0; Indels	APPLICANT: Board of Regents, The University of Texas System	
	0; Gaps	TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display	
	0; Indels	FILE REFERENCE: 005774.P003PCT	
	0; Gaps	CURRENT APPLICATION NUMBER: PCT/US01/27692A	
	0; Indels	CURRENT FILING DATE: 2001-09-07	
	0; Gaps	NUMBER OF SEQ ID NOS: 251	
	0; Indels	SOFTWARE: PatentIn version 3.1	
	0; Gaps	SEQ ID NO 161	
	0; Indels	LENGTH: 3	
	0; Gaps	TYPE: PRT	
	0; Indels	ORGANISM: Artificial Sequence	
	0; Gaps	NAME/KEY: Peptide	
	0; Indels	LOCATION: (1)..(3)	
	0; Gaps	OTHER INFORMATION: synthetic construct	
	0; Indels	PCT-US01-27692A-161	
	0; Gaps	Query Match	
	0; Indels	Best Local Similarity	
	0; Gaps	Matches	
	0; Indels	Score 4; DB 1; Length 3;	
	0; Gaps	Pred. No. 4.8e+04;	
	0; Indels	Mismatches 0; Indels 0; Gaps 0;	
	0; Indels	OY	
	0; Gaps	L L 1	
	0; Indels	Db	
	0; Gaps	3 L 3	
	0; Indels	RESULT 7	
	0; Gaps	PCT-US01-27692A-179	
	0; Indels	Sequence 179, Application PC/TUS0127692A	
	0; Gaps	GENERAL INFORMATION:	
	0; Indels	APPLICANT: Board of Regents, The University of Texas System	
	0; Gaps	TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display	
	0; Indels	FILE REFERENCE: 005774.P003PCT	
	0; Gaps	CURRENT APPLICATION NUMBER: PCT/US01/27692A	
	0; Indels	CURRENT FILING DATE: 2001-09-07	
	0; Gaps	NUMBER OF SEQ ID NOS: 251	
	0; Indels	SOFTWARE: PatentIn version 3.1	
	0; Gaps	SEQ ID NO 138	
	0; Indels	LENGTH: 3	
	0; Gaps	TYPE: PRT	
	0; Indels	ORGANISM: Artificial Sequence	
	0; Gaps	NAME/KEY: Peptide	
	0; Indels	LOCATION: (1)..(3)	
	0; Gaps	OTHER INFORMATION: synthetic construct	
	0; Indels	PCT-US01-27692A-138	
	0; Gaps	Query Match	
	0; Indels	Best Local Similarity	
	0; Gaps	Matches	
	0; Indels	Score 4; DB 1; Length 3;	
	0; Gaps	Pred. No. 4.8e+04;	
	0; Indels	Mismatches 0; Indels 0; Gaps 0;	
	0; Indels	OY	
	0; Gaps	L L 1	
	0; Indels	Db	
	0; Gaps	3 L 3	
	0; Indels	US-09-934-101	
	0; Gaps	Sequence 101, Application US/09720934	
	0; Indels	GENERAL INFORMATION:	
	0; Gaps	APPLICANT: Korenberg, Julie R	
	0; Indels	APPLICANT: Chen, Xiao-Ning	
	0; Gaps	TITLE OF INVENTION: ISOLATED SH3 GENES ASSOCIATED WITH MYELOPROLIFERATIVE	
	0; Indels	TITLE OF INVENTION: DISORDERS AND LEUKEMIA, AND USES THEREOF	
	0; Gaps	FILE REFERENCE: 2320-1-001PCT	
	0; Indels	CURRENT APPLICATION NUMBER: US/09/720,934	
	0; Gaps	CURRENT FILING DATE: 2001-10-03	
	0; Indels	PRIOR APPLICATION NUMBER: 60/082,007	
	0; Gaps	PRIOR FILING DATE: 1998-04-16	
	0; Indels	NUMBER OF SEQ ID NOS: 109	
	0; Gaps	SOFTWARE: PatentIn Ver. 2.0	
	0; Indels	SEQ ID NO 101	
	0; Gaps	LENGTH: 2	
	0; Indels	TYPE: PRT	
	0; Gaps	ORGANISM: Homo sapiens	
	0; Indels	US-09-720-934-101	
	0; Gaps	Query Match	
	0; Indels	Best Local Similarity	
	0; Gaps	Matches	
	0; Indels	Score 4; DB 5; Length 2;	
	0; Gaps	Pred. No. 4.8e+04;	
	0; Indels	Mismatches 0; Indels 0; Gaps 0;	
	0; Indels	OY	
	0; Gaps	L L 1	
	0; Indels	Db	
	0; Gaps	2 L 2	
	0; Indels	RESULT 4	
	0; Gaps	PCT-US01-27692A-138	
	0; Indels	Sequence 138, Application PC/TUS0127692A	
	0; Gaps	GENERAL INFORMATION:	
	0; Indels	APPLICANT: Board of Regents, The University of Texas System	
	0; Gaps	TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display	
	0; Indels	FILE REFERENCE: 005774.P003PCT	
	0; Gaps	CURRENT APPLICATION NUMBER: PCT/US01/27692A	
	0; Indels	CURRENT FILING DATE: 2001-09-07	
	0; Gaps	NUMBER OF SEQ ID NOS: 251	
	0; Indels	SOFTWARE: PatentIn version 3.1	
	0; Gaps	SEQ ID NO 138	
	0; Indels	LENGTH: 3	
	0; Gaps	TYPE: PRT	
	0; Indels	ORGANISM: Artificial Sequence	
	0; Gaps	NAME/KEY: Peptide	
	0; Indels	LOCATION: (1)..(3)	
	0; Gaps	OTHER INFORMATION: synthetic construct	
	0; Indels	PCT-US01-27692A-138	
	0; Gaps	Query Match	
	0; Indels	Best Local Similarity	
	0; Gaps	Matches	
	0; Indels	Score 4; DB 1; Length 3;	
	0; Gaps	Pred. No. 4.8e+04;	
	0; Indels	Mismatches 0; Indels 0; Gaps 0;	
	0; Indels	OY	
	0; Gaps	L L 1	
	0; Indels	Db	
	0; Gaps	3 L 3	

; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 179  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; NAME/KEY: Peptide  
; LOCATION: (1)..(3)  
; OTHER INFORMATION: synthetic construct  
PCT-US01-27692A-179

Query Match 36.4%; Score 4; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 4.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
DB 2 L 2

RESULT 8  
PCT-US01-27692A-181  
; Sequence 181, Application PC/TUS0127692A  
; GENERAL INFORMATION:  
; APPLICANT: Board of Regents, The University of Texas System  
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display  
; FILE REFERENCE: 005774.P003PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/27692A  
; CURRENT FILING DATE: 2001-09-07  
; NUMBER OF SEQ ID NOS: 251  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 181  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; NAME/KEY: Peptide  
; LOCATION: (1)..(3)  
; OTHER INFORMATION: synthetic construct  
PCT-US01-27692A-181

Query Match 36.4%; Score 4; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 4.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
DB 2 L 2

RESULT 9  
PCT-US01-28044A-8  
; Sequence 8, Application PC/TUS0128044A  
; GENERAL INFORMATION:  
; APPLICANT: Board of Regents, The University of Texas System  
; TITLE OF INVENTION: Compositions and Methods for Targeting Peptide in Human In Vivo  
; FILE REFERENCE: 005774.P002PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/28044A  
; CURRENT FILING DATE: 2001-09-07  
; NUMBER OF SEQ ID NOS: 423  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; NAME/KEY: Peptide  
; LOCATION: (1)..(3)  
; OTHER INFORMATION: synthetic construct  
PCT-US01-28044A-8

Query Match 36.4%; Score 4; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 4.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
DB 1 L 1

RESULT 10  
PCT-US01-28044A-9  
; Sequence 9, Application PC/TUS0128044A  
; GENERAL INFORMATION:  
; APPLICANT: Board of Regents, The University of Texas System  
; TITLE OF INVENTION: Compositions and Methods for Targeting Peptide in Human In Viv  
; FILE REFERENCE: 005774.P002PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/28044A  
; CURRENT FILING DATE: 2001-09-07  
; NUMBER OF SEQ ID NOS: 423  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; NAME/KEY: Peptide  
; LOCATION: (1)..(3)  
; OTHER INFORMATION: synthetic construct  
PCT-US01-28044A-9

Query Match 36.4%; Score 4; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 4.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
DB 1 L 1

RESULT 11  
PCT-US01-28044A-10  
; Sequence 10, Application PC/TUS0128044A  
; GENERAL INFORMATION:  
; APPLICANT: Board of Regents, The University of Texas System  
; TITLE OF INVENTION: Compositions and Methods for Targeting Peptide in Human In Viv  
; FILE REFERENCE: 005774.P002PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/28044A  
; CURRENT FILING DATE: 2001-09-07  
; NUMBER OF SEQ ID NOS: 423  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; NAME/KEY: Peptide  
; LOCATION: (1)..(3)  
; OTHER INFORMATION: synthetic construct  
PCT-US01-28044A-10

Query Match 36.4%; Score 4; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 4.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
DB 1 L 1

RESULT 12



```
PCT-US01-28044A-15
; Sequence 15, Application PC/TUS0128044A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Compositions and Methods for Targeting Peptide in Human In Vivo
; FILE REFERENCE: 005774.P002PCT
; CURRENT APPLICATION NUMBER: PCT/US01/28044A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: Peptide
; LOCATION: (1)..(3)
; OTHER INFORMATION: synthetic construct
PCT-US01-28044A-15

Query Match          36.4%; Score 4; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 4.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1
Db 3 L 3

RESULT 13
PCT-US01-28044A-21
; Sequence 21, Application PC/TUS0128044A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Compositions and Methods for Targeting Peptide in Human In Vivo
; FILE REFERENCE: 005774.P002PCT
; CURRENT APPLICATION NUMBER: PCT/US01/28044A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: Peptide
; LOCATION: (1)..(3)
; OTHER INFORMATION: synthetic construct
PCT-US01-28044A-21

Query Match          36.4%; Score 4; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 4.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1
Db 3 L 3

RESULT 14
PCT-US01-28044A-130
; Sequence 130, Application PC/TUS0128044A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Compositions and Methods for Targeting Peptide in Human In Vivo
; FILE REFERENCE: 005774.P002PCT
; CURRENT APPLICATION NUMBER: PCT/US01/28044A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
```

```
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(3)
; OTHER INFORMATION: synthetic construct
PCT-US01-28044A-130

Query Match          36.4%; Score 4; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 4.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1
Db 1 L 1

RESULT 15
PCT-US01-28044A-306
; Sequence 306, Application PC/TUS0128044A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Compositions and Methods for Targeting Peptide in Human In Vivo
; FILE REFERENCE: 005774.P002PCT
; CURRENT APPLICATION NUMBER: PCT/US01/28044A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 306
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: Peptide
; LOCATION: (1)..(3)
; OTHER INFORMATION: synthetic construct
PCT-US01-28044A-306

Query Match          36.4%; Score 4; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 4.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1
Db 1 L 1

Search completed: December 13, 2001, 10:49:47
Job time: 307 sec
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us-09-424-080a-1.closed.ra1

Thu Dec '13 12:06:07 2001

OM protein - protein search, using sw model  
Run on: December 13, 2001, 11:55:36 ; Search time 20.43 Seconds  
(without alignments)  
8.812 Million cell updates/sec

Title: US-09-424-080A-1  
Perfect score: 42  
Sequence: 1: LTERKYP 8  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues 8027  
Total number of hits satisfying chosen parameters:  
Minimum DB seq length: 8  
Maximum DB seq length: 8  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*  
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4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42.0	100.0	8	2	US-08-669-284B-30
2	21	50.0	8	4	US-08-444-818-659
3	20	47.6	8	1	US-08-178-570-47
4	20	47.6	8	3	US-08-369-643-47
5	20	47.6	8	5	PCT-US95-00147-47
6	19	45.2	8	1	US-08-178-570-48
7	19	45.2	8	3	US-08-369-643-48
8	19	45.2	8	5	PCT-US95-00147-48
9	19	45.2	8	6	PCT-US95-00147-44
10	18	42.9	8	1	US-08-082-847-7
11	18	42.9	8	1	US-08-082-847-9
12	18	42.9	8	1	US-08-082-847-29
13	18	42.9	8	1	US-08-375-962B-2
14	18	42.9	8	2	US-08-615-181-67
15	18	42.9	8	2	US-08-978-404B-62
16	18	42.9	8	3	US-08-562-114B-2
17	18	42.9	8	3	US-08-478-208-18
18	18	42.9	8	4	US-08-444-818-734
19	18	42.9	8	4	US-08-444-818-735
20	18	42.9	8	4	US-08-444-818-736
21	18	42.9	8	4	US-08-444-818-737
22	18	42.9	8	4	US-08-861-423A-9
23	18	42.9	8	4	US-07-861-458C-121
24	18	42.9	8	4	US-08-729-594A-2
25	18	42.9	8	5	PCT-US95-02140-1
26	17	40.5	8	1	US-08-236-240-3
27	17	40.5	8	1	US-08-266-514-12

28	17	40.5	8	2	US-08-654-604-12
29	17	40.5	8	2	US-08-934-222-140
30	17	40.5	8	2	US-08-669-284B-13
31	17	40.5	8	2	US-08-669-284B-14
32	17	40.5	8	2	US-08-669-284B-15
33	17	40.5	8	2	US-08-933-402-140
34	17	40.5	8	2	US-09-207-621-140
35	17	40.5	8	2	US-08-350-260A-466
36	17	40.5	8	2	US-08-532-818-140
37	17	40.5	8	3	US-09-231-797-140
38	17	40.5	8	3	US-08-934-224-140
39	17	40.5	8	3	US-08-933-843-140
40	17	40.5	8	4	US-08-934-223-140
41	17	40.5	8	4	US-08-444-818-660
42	17	40.5	8	4	US-09-171-654-23
43	17	40.5	8	4	US-09-413-492-140
44	16	38.1	8	1	US-08-178-570-50
45	16	38.1	8	1	US-08-259-550A-30

ALIGNMENTS

RESULT 1  
US-08-669-284B-30  
; Sequence 30, Application US/08669284B  
; Patent No. 5939534  
; GENERAL INFORMATION:  
; APPLICANT: Inoue, Makoto  
; APPLICANT: Kikuchi, Kaoru  
; APPLICANT: Ishige, Yoko  
; APPLICANT: Kimura, Toru  
; APPLICANT: Nakayama, Chikao  
; APPLICANT: No. 5939534uchi, Hiroshi  
; TITLE OF INVENTION: NOVEL HUMAN CILIARY NEUTROTROPHIC FACTORS  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/669,284B  
FILING DATE: 28-JUN-1996  
PRIOR APPLICATION DATA: PCT/JP94/02269  
APPLICATION NUMBER: PCT/JP94/02269  
FILING DATE: 27-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 06-268281  
FILING DATE: 05-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 06-201504  
FILING DATE: 02-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 05-350934  
FILING DATE: 29-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Nakamura, Dean H.  
REGISTRATION NUMBER: 33,981  
REFERENCE/DOCKET NUMBER: Q-42041  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:

SEQ ID NO: 30

LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-659-284B-30

Query Match 100.0%; Score 42; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTKKYSP 8  
DB 1 LTKKYSP 8

RESULT 2  
US-08-444-818-659

; Sequence 659, Application US/08444818  
; Patent No. 6150087  
; GENERAL INFORMATION:  
; APPLICANT: Chien, David Y.  
; APPLICANT: Rutter, William J.  
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines  
; NUMBER OF SEQUENCES: 777  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Chiron Corporation  
; STREET: 4560 Horton Street  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608-2916  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444,818  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/403,590  
; FILING DATE: 14-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Harbin, Alisa A.  
; REGISTRATION NUMBER: 33,895  
; REFERENCE/DOCKET NUMBER: 0110.002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (508)359-3876  
; TELEFAX: (508)359-3885 659:  
; INFORMATION FOR SEQ ID NO:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-444-818-659

Query Match 50.0%; Score 21; DB 4; Length 8;  
Best Local Similarity 66.7%; Pred. No. 1.6e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTKKY 6  
DB 1 LTKLY 6

RESULT 3  
US-08-178-570-47

; Sequence 47, Application US/08178570  
; Patent No. 5532167  
; GENERAL INFORMATION:  
; APPLICANT: Lewis C. Cantley  
; APPLICANT: Zhou Song Yang  
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 STATE STREET, suite 510  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/178,570  
; FILING DATE: JANUARY 7, 1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Decontt, Giulio A. Jr.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: BBI-004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941 47:  
; INFORMATION FOR SEQ ID NO:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-08-178-570-47

Query Match 47.6%; Score 20; DB 1; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.6e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EKKYSP 8  
DB 1 EEEYMP 6

RESULT 4

US-08-369-643-47  
; Sequence 47, Application US/08369643A  
; Patent No. 6004757  
; GENERAL INFORMATION:  
; APPLICANT: Cantley, Lewis C.  
; APPLICANT: Songyang, Zhou  
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases  
; FILE REFERENCE: CNS-001CP  
; CURRENT APPLICATION NUMBER: US/08/369,643A  
; CURRENT FILING DATE: 1995-01-06  
; EARLIER APPLICATION NUMBER: US 08/178,570  
; EARLIER FILING DATE: 1994-01-07  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 47  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Mouse polyoma  
; OTHER INFORMATION: middle T (Y315)  
US-08-369-643-47

us-09-424-080a-1.closed.ra1

Thu Dec '13 12:06:07 2001

Query Match 47.6%; Score 20; DB 3; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.6e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EKKYSP 8  
1:1:1  
Db 1 ENEYMP 6

RESULT 5  
PCT-US95-00147-47  
Sequence 47, Application PC/TUS9500147  
GENERAL INFORMATION:  
APPLICANT: Substrate Specificity of Protein Kinases  
TITLE OF INVENTION: 88  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 STATE STREET, suite 510  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/00147  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/178,570  
FILING DATE: JANUARY 7, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A., Jr.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: BBI-004CPPC  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
PCT-US95-00147-47

Query Match 47.6%; Score 20; DB 5; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.6e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EKKYSP 8  
1:1:1  
Db 1 ENEYMP 6

RESULT 6  
US-08-178-570-48  
Sequence 48, Application US/08178570  
Patent No. 5532167  
GENERAL INFORMATION:  
APPLICANT: Lewis C. Cantley  
TITLE OF INVENTION: Substrate Specificity of Protein Kinases  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 STATE STREET, suite 510

CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/178,570  
FILING DATE: JANUARY 7, 1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A., Jr.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: BBI-004  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-178-570-48

Query Match 45.2%; Score 19; DB 1; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.6e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKKYSP 8  
1:1:1  
Db 1 ENEYMP 6

RESULT 7  
US-08-369-643-48  
Sequence 48, Application US/08369643A  
Patent No. 6004757  
GENERAL INFORMATION:  
APPLICANT: Cantley, Lewis C.  
TITLE OF INVENTION: Substrate Specificity of Protein Kinases  
FILE REFERENCE: CNS-001CP  
CURRENT APPLICATION NUMBER: US/08/369,643A  
CURRENT FILING DATE: 1995-01-06  
EARLIER FILING DATE: 1994-01-07  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 48  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Hamster  
OTHER INFORMATION: polyoma middle T (Y295)  
US-08-369-643-48

Query Match 45.2%; Score 19; DB 3; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.6e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKKYSP 8  
1:1:1  
Db 1 ENEYMP 6

RESULT 8  
PCT-US95-00147-48  
; Sequence 48, Application PC/TUS9500147  
; GENERAL INFORMATION:  
; APPLICANT: Substrate Specificity of Protein Kinases  
; TITLE OF INVENTION: 88  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 STATE STREET, suite 510  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/00147  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/178,570  
; FILING DATE: JANUARY 7, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A., Jr.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: BBI-004CPPC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
PCT-US95-00147-48

Query Match 45.2%; Score 19; DB 5; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.6e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 3 EKKYSP 8  
Db 1 ENEYMP 6

RESULT 9  
5258287-44  
; Patent No. 5258287  
; APPLICANT: BAXTER, ROBERT C.; WOOD, WILLIAM I.  
; TITLE OF INVENTION: DNA ENCODING AND METHODS OF PRODUCTION  
; OF INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN BP53  
; NUMBER OF SEQUENCES: 58  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/171,623  
; FILING DATE: 22-MAR-1988  
; SEQ ID NO: 44:  
; LENGTH: 8  
5258287-44

Query Match 45.2%; Score 19; DB 6; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.6e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 3 EKKYSP 8  
Db 1 ENEYGP 6

RESULT 10  
US-08-082-847-7  
; Sequence 7, Application US/08082847  
; Patent No. 5492894  
; GENERAL INFORMATION:  
; APPLICANT: FULMER, ANDREW W.  
; APPLICANT: BASCOM, CHARLES C.  
; TITLE OF INVENTION: COMPOSITIONS FOR REGULATING WRINKLES  
; TITLE OF INVENTION: COMPRISING A PEPTIDE  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: THE PROCTER & GAMBLE COMPANY  
; STREET: P. O. BOX 398707  
; CITY: CINCINNATI  
; STATE: OHIO  
; COUNTRY: USA  
; ZIP: 45239-8707  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/082,847  
; FILING DATE: 19930625  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CORSTANJE, BRAHM J.  
; REGISTRATION NUMBER: 34,804  
; REFERENCE/DOCKET NUMBER: 4346CR  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 513-627-2858  
; TELEFAX: 513-627-0260  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-082-847-7

Query Match 42.9%; Score 18; DB 1; Length 8;  
Best Local Similarity 75.0%; Pred. No. 1.6e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 4 KKYS 7  
Db 5 RKYS 8

RESULT 11  
US-08-082-847-9  
; Sequence 9, Application US/08082847  
; Patent No. 5492894  
; GENERAL INFORMATION:  
; APPLICANT: FULMER, ANDREW W.  
; APPLICANT: BASCOM, CHARLES C.  
; TITLE OF INVENTION: COMPOSITIONS FOR REGULATING WRINKLES  
; TITLE OF INVENTION: COMPRISING A PEPTIDE  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: THE PROCTER & GAMBLE COMPANY  
; STREET: P. O. BOX 398707  
; CITY: CINCINNATI  
; STATE: OHIO  
; COUNTRY: USA  
; ZIP: 45239-8707  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

us-09-424-080a-1.closed.ra1

Thu Dec '13 12:06:07 2001

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/082,847  
 FILING DATE: 19930625  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: CORSTANJE, BRAHM J.  
 REGISTRATION NUMBER: 34,804  
 REFERENCE/DOCKET NUMBER: 4346CR  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 513-627-2858  
 TELEFAX: 513-627-0260  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-082-847-9

Query Match 42.9%; Score 18; DB 1; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 1.6e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KAYS 7  
 DB 5 RKYS 8

RESULT 12  
 US-08-082-847-29  
 Sequence 29, Application US/08082847  
 Patent No. 5492894  
 GENERAL INFORMATION:  
 APPLICANT: FULMER, ANDREW W.  
 APPLICANT: BASCOM, CHARLES C.  
 TITLE OF INVENTION: COMPOSITIONS FOR REGULATING WRINKLES  
 TITLE OF INVENTION: COMPRISING A PEPTIDE  
 NUMBER OF SEQUENCES: 38  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: THE PROCTER & GAMBLE COMPANY  
 STREET: P. O. BOX 398707  
 CITY: CINCINNATI  
 STATE: OHIO  
 COUNTRY: USA  
 ZIP: 45239-8707  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/082,847  
 FILING DATE: 19930625  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: CORSTANJE, BRAHM J.  
 REGISTRATION NUMBER: 34,804  
 REFERENCE/DOCKET NUMBER: 4346CR  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 513-627-2858  
 TELEFAX: 513-627-0260  
 INFORMATION FOR SEQ ID NO: 29:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-082-847-29

Query Match 42.9%; Score 18; DB 1; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 1.6e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KAYS 7  
 DB 4 RKYS 7

RESULT 13  
 US-08-375-962B-2  
 Sequence 2, Application US/08375962B  
 Patent No. 5731195  
 GENERAL INFORMATION:  
 APPLICANT: SIMON, ANDRAS; HELLMAN, ULF; WERNSTEDT,  
 APPLICANT: CHRISTER, ERIKSSON, ULF.  
 TITLE OF INVENTION: Isolated Nucleic Acid Molecule  
 TITLE OF INVENTION: Which Codes for A 32 Kda Protein Having 11-Cis Retinol  
 TITLE OF INVENTION: Dehydrogenase Activity, and Which Associates With P63,  
 TITLE OF INVENTION: a Portion of a Retinol Binding Protein Receptor  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pelfe & Lynch  
 STREET: 805 Third Avenue  
 CITY: New York City  
 STATE: New York  
 ZIP: 10022  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage  
 COMPUTER: IBM  
 OPERATING SYSTEM: PC-DOS  
 SOFTWARE: Wordperfect (ASCII standard)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/375,962B  
 FILING DATE: 20-January-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/258,418  
 FILING DATE: 6-October-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pasqualini, Patricia A.  
 REGISTRATION NUMBER: 34,894  
 REFERENCE/DOCKET NUMBER: LUD 5372.1 CIP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 688-9200  
 TELEFAX: (212) 838-3884  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-375-962B-2

Query Match 42.9%; Score 18; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YSP 8  
 DB 1 YSP 3

RESULT 14  
 US-08-615-181-67  
 Sequence 67, Application US/08615181  
 Patent No. 5756666  
 GENERAL INFORMATION:  
 APPLICANT: MASAFUMI, TAKIGUCHI  
 APPLICANT: MIWA, KIYOSHI  
 TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING IMMUNE

TITLE OF INVENTION: RESPONSE TO HIV AND ANTI-AIDS AGENT FOR PREVENTING AND  
TITLE OF INVENTION: CURING AIDS  
NUMBER OF SEQUENCES: 115  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT,  
P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/615,181  
FILING DATE: 04-APR-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP94/01756  
FILING DATE: 19-OCT-1993  
APPLICATION NUMBER: JP 261302/1993  
FILING DATE: 19-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-796-0 PCT  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
ORIGINAL SOURCE: HUMAN IMMUNODEFICIENCY VIRUS  
US-08-615-181-67

Query Match 42.9%; Score 18; DB 1; Length 8;  
Best Local Similarity 75.0%; Pred. No. 1.6e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EKKY 6  
DB 5 KKKY 8

RESULT 15  
US-08-978-404B-62  
Sequence 62, Application US/08978404B  
Patent No. 5968782  
GENERAL INFORMATION:  
APPLICANT: Stevens, Richard L.  
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES  
TITLE OF INVENTION: FIBRINOGEN  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: MA  
COUNTRY: U.S.A.  
ZIP: 02210-2211  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/978,404B  
FILING DATE: 25-NOV-97  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/032,354  
FILING DATE: 04-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Plumer, Elizabeth R.  
REGISTRATION NUMBER: 36,637  
REFERENCE/DOCKET NUMBER: B0801/7090  
TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 5968782e  
US-08-978-404B-62

Query Match 42.9%; Score 18; DB 2; Length 8;  
Best Local Similarity 57.1%; Pred. No. 1.6e+05;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TEKKYSP 8  
DB 2 TPTKLSP 8

Search completed: December 13, 2001, 11:56:05  
Job time: 29 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 13, 2001, 10:44:40 ; Search time 22.81 Seconds  
(without alignments)  
26.716 Million cell updates/sec

Title: us-09-424-080a-1

Perfect score: 42

Sequence: 1 LTERKYP 8

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	72	2 I79343	interferon alpha-T
2	42	100.0	167	2 E25843	interferon alpha-F
3	42	100.0	167	2 D25843	interferon alpha-G
4	42	100.0	176	2 I36314	interferon alpha-2
5	42	100.0	181	2 I36313	interferon alpha-1
6	42	100.0	189	1 IVH016	interferon alpha-1
7	42	100.0	189	1 IVH0A7	interferon alpha-5
8	42	100.0	189	1 IVH0A1	interferon alpha-1
9	42	100.0	189	1 IVH0F	interferon alpha-1
10	42	100.0	189	1 IVH0A8	interferon alpha-1
11	42	100.0	189	2 I52347	interferon alpha-M
12	42	100.0	189	2 I34464	interferon alpha-F
13	42	100.0	189	2 I53102	interferon alpha-J
14	42	100.0	189	2 I51970	interferon precurs
15	42	100.0	189	2 I78570	alpha 2 interferon
16	36	85.7	165	2 F25843	interferon, atypic
17	36	85.7	167	2 A48772	interferon, atypic
18	36	85.7	170	2 IVH0A2	interferon alpha-1
19	36	85.7	184	1 IVH0A2	interferon alpha-1
20	36	85.7	184	1 IVH0A1	interferon alpha-1
21	36	85.7	184	1 IVH0A1	interferon alpha-1
22	36	85.7	184	1 IVH0A1	interferon alpha-1
23	36	85.7	188	1 IVH0A2	interferon alpha-2
24	36	85.7	189	1 IVH0A4	interferon alpha-1
25	36	85.7	189	1 IVH0A0	interferon precurs
26	36	85.7	194	2 J50664	interferon alpha-B
27	36	85.7	730	2 H62955	hypothetical prote
28	35	83.3	162	2 C25843	interferon alpha-4
29	35	83.3	189	1 IVH0A4	interferon alpha-4

interferon alpha-1  
interferon alpha-1  
hypothetical prote  
interferon alpha-5  
hypothetical prote  
immunomodulatory p  
protein TNF15.3 (1  
hypothetical prote  
ATPase homolog-- C  
interferon alpha-1  
interferon alpha-1  
interferon alpha-1  
murine interferon  
interferon alpha-2  
interferon alpha-1

## ALIGNMENTS

### RESULT 1

I79343

Interferon alpha T - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 16-Jul-1999

C:Accession: I79343

R:Lund, B.; Edlund, T.; Lindenmaier, W.; Ny, T.; Collins, J.; Lundgren, E.; von Gabal

Proc. Natl. Acad. Sci. U.S.A. 81, 2435-2439, 1984

A:Title: Novel cluster of alpha-interferon gene sequences in a placental cosmid DNA 1

A:Reference number: I58999; MUID:84194022

A:Accession: I79343

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-72 <RES>

A:Cross-references: GB:K01461; NID:g184575; PIDN:AAA58685.1; PID:g184579

C:Superfamily: interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 72;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYP 8

DB 65 LTERKYP 72

### RESULT 2

E25843

Interferon alpha-F - human

N:Alternate names: human leukocyte interferon (IFN)

C:Species: Homo sapiens (man)

C:Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 15-Jun-1996

C:Accession: E25843

R:Ohara, O.; Teraoka, H.

FEBS Lett. 211, 78-82, 1987

A:Title: Anomalous behavior of human leukocyte interferon subtypes on polyacrylamide

A:Reference number: A91374; MUID:87105954

A:Accession: E25843

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-167 <OHA>

C:Superfamily: interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 167;  
Best Local Similarity 100.0%; Pred. No. 0.25; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0;

QY 1 LTERKYP 8

DB 132 LTERKYP 139



```

RESULT 3
Interferon alpha-G - human
N:Alternate names: human leukocyte interferon (IFN)
C:Species: Homo sapiens (man)
C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 15-Jun-1996
C:Accession: D25843
P:Ohara, O.; Teraoka, H.
FEBS Lett. 211:78-82, 1987
A:Title: Anomalous behavior of human leukocyte interferon subtypes on polyacrylamide gel
A:Reference number: A91374; MUID:87105954
A:Accession: D25843
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-167 <OHA>
C:Superfamily: Interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTKKYSKP 8
    |||||
DB 132 LTKKYSKP 139

RESULT 4
Interferon-alpha - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C:Accession: I56314
P:Lund, B.; von Gabain, A.; Edlund, T.; Ny, T.; Lundgren, E.
J. Interferon Res. 5: 229-238, 1985
A:Title: Differential expression of interferon genes in a substrain of Namalwa cells.
A:Reference number: I56314; MUID:85235859
A:Accession: I56314
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-176 <RES>
A:Cross-references: GB:M71246; NID:g184572; PIDN:AAA52713.1; PID:g184573
C:Genetics:
A:Gene: IFNA
C:Superfamily: Interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 176;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTKKYSKP 8
    |||||
DB 141 LTKKYSKP 148

RESULT 5
Interferon alpha 21 - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C:Accession: I56313
P:Gren, E.; Berzin, V.M.; Jansone, I.; Tsimanis, A.; Vishnevsky, Y.; Apsalons, U.
J. Interferon Res. 4: 609-617, 1984
A:Title: Novel human leukocyte interferon subtype and structural comparison of alpha 1
A:Reference number: I56313; MUID:85056523
A:Accession: I56313
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-181 <RES>
A:Cross-references: GB:M28586; NID:g184636; PIDN:AAA36041.1; PID:g306912

```

```

C:Genetics:
A:Gene: GDB:IFNA21
A:Cross-references: GDB:I36360; OMIM:147584
A:Map position: 9p22-9p22
C:Superfamily: Interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTKKYSKP 8
    |||||
DB 146 LTKKYSKP 153

RESULT 6
Interferon-alpha-I-6 precursor - human
N:Alternate names: HuIFN-alpha-I-6; LeIF K; type I interferon
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 18-Jun-1999
C:Accession: A23753
P:Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.;
J. Mol. Biol. 185, 227-260, 1985
A:Title: Structural relationship of human interferon alpha genes and pseudogenes.
A:Reference number: A92916; MUID:86037205
A:Accession: A23753
A:Molecule type: DNA
A:Residues: 1-189 <HEN>
A:Cross-references: GB:X02958; NID:g32662; PIDN:CAA26704.1; PID:g758080
C:Genetics:
A:Gene: GDB:IFNA6
A:Cross-references: GDB:I36363; OMIM:147566
A:Map position: 9p22-9p22
C:Superfamily: Interferon alpha
C:Keywords: antiviral
P:1-23/Domain: signal sequence #status predicted <SIG>
P:24-189/Product: interferon alpha-I-6 #status predicted <MAT>
P:24-122,52-162/Disulfide bonds: #status predicted

Query Match 100.0%; Score 42; DB 1; Length 189;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTKKYSKP 8
    |||||
DB 154 LTKKYSKP 161

RESULT 7
Interferon alpha-5 precursor - human
N:Alternate names: Interferon alpha-G
C:Species: Homo sapiens (man)
C:Date: 01-Sep-1981 #sequence_revision 29-Jan-1999 #text_change 21-Jul-2000
C:Accession: S43716; A01833
P:Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.;
J. Mol. Biol. 185, 227-260, 1985
A:Title: Structural relationship of human interferon alpha genes and pseudogenes.
A:Reference number: A92916; MUID:86037205
A:Accession: S43716
A:Molecule type: DNA
A:Residues: 1-189 <HEN>
A:Cross-references: EMBL:X02956; NID:g32659; PIDN:CAA26704.1; PID:g758079
P:Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandliss, R.; Seeb
Nature 290, 20-26, 1981
A:Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.
A:Reference number: A93249; MUID:81148795
A:Accession: A01833
A:Molecule type: mRNA
A:Residues: 57-189 <GOE>

```

A;Cross-references: GB:V00541; GB:J00213; NID:g32718; PIDN:CAA23802.1; PID:g32719  
A;Note: eight classes of interferon alpha clones were identified; this sequence is derived from  
C;Genetics:  
A;Gene: GDB:IFNA5  
A;Cross-references: GDB:136362; OMIM:147565  
A;Map position: 9p22-9p22  
C;Superfamily: interferon alpha  
C;Keywords: antiviral; cytokine; leukocyte  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-189/Product: interferon alpha-5 #status predicted <MAT>  
Query Match 100.0%; Score 42; DB 1; Length 189;  
Best Local Similarity 100.0%; Pred. No. 0.28; 0; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LTERKYSKP 8  
DB 154 LTERKYSKP 161  
RESULT 8  
IVH041  
N;Alternate names: interferon alpha-1 precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 22-May-1981 #sequence\_revision 01-Sep-1981 #text\_change 24-Sep-1999  
C;Accession: C23285; A91467; A93226; A93249; I58213; S43715; S41196; A01826  
R;Capon, D.J.; Shepard, H.M.; Goeddel, D.V.  
Mol. Cell. Biol. 5, 768-779, 1985  
A;Title: Two distinct families of human and bovine interferon-alpha genes are coordinately  
A;Reference number: A93070; MUID:85187974  
A;Accession: C23285  
A;Molecule type: DNA  
A;Residues: 1-189 <CAP>  
R;Watanabe, N.; Schwarzstein, M.; Streuli, M.; Panem, S.; Nagata, S.; Weissmann, C.  
Gene 10, 1-10, 1980  
A;Title: The nucleotide sequence of a cloned human leukocyte interferon cDNA.  
A;Reference number: A91467; MUID:81005094  
A;Accession: A91467  
A;Molecule type: mRNA  
A;Residues: 1-189 <MAN>  
A;Cross-references: GB:V00537; NID:g32711; PIDN:CAA23798.1; PID:g32712  
R;Taniguchi, T.; Mantel, N.; Schwarzstein, M.; Nagata, S.; Muramatsu, M.; Weissmann, C.  
Nature 285, 547-549, 1980  
A;Title: Human leukocyte and fibroblast interferons are structurally related.  
A;Reference number: A93226; MUID:80254543  
A;Accession: A93226  
A;Molecule type: mRNA  
A;Residues: 1-189 <TAN>  
R;Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; McCandliss, R.; Seeburg  
Nature 290, 20-26, 1981  
A;Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.  
A;Reference number: A93249; MUID:81148795  
A;Accession: A93249  
A;Molecule type: mRNA  
A;Residues: 1-136, 'V', 138-189 <GOE>  
A;Cross-references: GB:V00538; NID:g32713; PIDN:CAA23799.1; PID:g32714  
A;Note: eight classes of interferon alpha clones were identified; this sequence is derived from  
R;Weber, H.; Weissmann, C.  
Nucleic Acids Res. 11, 5661-5669, 1983  
A;Title: Formation of genes coding for hybrid proteins by recombination between related.  
A;Reference number: I58213; MUID:83299241  
A;Accession: I38213  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 24-189 <RES>  
A;Cross-references: GB:M29884; NID:g184583; PIDN:AAA52714.1; PID:g386794  
R;Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.; Kov  
J. Mol. Biol. 185, 227-260, 1985  
A;Title: Structural relationship of human interferon alpha genes and pseudogenes.  
A;Reference number: A92916; MUID:86037205  
A;Accession: S43715

A;Molecule type: DNA  
A;Residues: 1-189 <HEN>  
A;Cross-references: EMBL:X75934  
R;Rostoks, N.  
submitted to the EMBL Data Library, December 1993  
A;Reference number: S41196  
A;Accession: S41196  
A;Molecule type: DNA  
A;Residues: 1-9, 'A', 11-189 <ROS>  
A;Cross-references: EMBL:X75934; NID:g439666; PIDN:CAA53538.1; PID:g439667  
C;Genetics:  
A;Gene: GDB:IFNA1  
A;Cross-references: GDB:136353; OMIM:147660  
A;Map position: 9p22-9p22  
C;Superfamily: interferon alpha  
C;Keywords: antiviral; cytokine; leukocyte  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-189/Product: interferon alpha-1 #status predicted <MAT>  
F;24-122,52-162/Disulfide bonds: #status predicted  
Query Match 100.0%; Score 42; DB 1; Length 189;  
Best Local Similarity 100.0%; Pred. No. 0.28; 0; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LTERKYSKP 8  
DB 154 LTERKYSKP 161  
RESULT 9  
IVH04F  
N;Alternate names: HuIFN-alpha-I-F; LeIF F; type I interferon  
C;Species: Homo sapiens (man)  
C;Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 28-May-1999  
C;Accession: A01832  
R;Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandliss, R.; Seeb  
Nature 290, 20-26, 1981  
A;Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.  
A;Reference number: A93249; MUID:81148795  
A;Accession: A01832  
A;Molecule type: mRNA  
A;Residues: 1-189 <GOE>  
A;Cross-references: GB:V00540; GB:J00212; NID:g32716; PIDN:CAA23801.1; PID:g32717  
A;Note: eight classes of interferon alpha clones were identified; this sequence is de  
C;Genetics:  
A;Gene: GDB:IFN1e  
A;Cross-references: GDB:119328; OMIM:147660  
A;Map position: 9p22-9p22  
C;Superfamily: interferon alpha  
C;Keywords: antiviral  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-189/Product: interferon alpha-I-F #status predicted <MAT>  
F;24-122,52-162/Disulfide bonds: #status predicted  
Query Match 100.0%; Score 42; DB 1; Length 189;  
Best Local Similarity 100.0%; Pred. No. 0.28; 0; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LTERKYSKP 8  
DB 154 LTERKYSKP 161  
RESULT 10  
IVH04B  
N;Alternate names: HuIFN-alpha-I-4b; type I interferon  
C;Species: Homo sapiens (man)  
C;Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 18-Jun-1999  
C;Accession: E23753

R:Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.; Kov  
J. Mol. Biol. 185, 227-260, 1985  
A:Title: Structural relationship of human interferon alpha genes and pseudogenes.  
A:Reference number: A92916; MUID:86037205  
A:Accession: E23753  
A:Molecule type: DNA  
A:Residues: 1-189 <HEN>  
A:Cross-references: GB:X02955; NID:g32656; PIDN:CAA26701.1; PID:g758078  
C:Genetics: IFN18  
A:Gene: GDB:IFN18  
A:Cross-references: GDB:119328; OMIM:147660  
A:Map position: 9p22-9p22  
C:Superfamily: Interferon alpha  
C:Keywords: antiviral  
F:1-23/domain: signal sequence #status predicted <SIG>  
F:24-189/Product: Interferon alpha-I-4b #status predicted <MAT>  
F:24-122,52-162/Disulfide bonds: #status predicted

Query Match 100.0%; Score 42; DB 1; Length 189;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTKKYSP 8  
DB 154 LTKKYSP 161  
|||||

RESULT 11  
IVHUA9  
Interferon alpha-17 precursor - human  
N:Alternate names: Interferon alpha-9; Interferon alpha-I'  
C:Species: Homo sapiens (man)  
C:Date: 01-Sep-1991 #sequence\_revision 01-Sep-1981 #text\_change 21-Jul-2000  
C:Accession: A01835; A22255; C42753  
R:Law, R.M.; Adelman, J.; Dull, T.J.; Gross, M.; Goeddel, D.; Ullrich, A.  
Science 212, 1159-1162, 1981  
A:Title: DNA sequence of two closely linked human leukocyte interferon genes.  
A:Reference number: A94255; MUID:81201124  
A:Accession: A01835  
A:Molecule type: DNA  
A:Residues: 1-189 <LAW>  
A:Cross-references: GB:J00216; GB:V00532; NID:g32633; PIDN:CAA23793.1; PID:g32634  
R:Mizoguchi, J.; Pitha, P.M.; Raj, N.B.K.  
DNA 4, 221-232, 1985  
A:Title: Efficient expression in Escherichia coli of two species of human interferon-  
A:Reference number: A22255; MUID:85229953  
A:Accession: A22255  
A:Molecule type: mRNA  
A:Residues: 1-56, 'H', 58-189 <MI>  
A:Cross-references: GB:M1026; NID:g184612; PIDN:AAA52725.1; PID:g306908  
R:Zoon, K.C.; Miller, D.; Bekisz, J.; zur Nedden, D.; Enterline, J.C.; Nguyen, N.Y.; Hu,  
J. Biol. Chem. 267, 15210-15216, 1992  
A:Title: Purification and characterization of multiple components of human lymphoblasto-  
A:Reference number: A42753; MUID:92340576  
A:Accession: C42753  
A:Molecule type: protein  
A:Residues: 'X', 25-50, 'YX', 53-56 <ZOO>  
C:Genetics:  
A:Gene: GDB:IFN17  
A:Cross-references: GDB:136358; OMIM:147583  
A:Map position: 9p22-9p22  
C:Superfamily: Interferon alpha  
C:Keywords: leukocyte  
F:1-23/domain: signal sequence #status predicted <SIG>  
F:24-189/Product: Interferon alpha-17 #status predicted <MAT>  
F:24-122,52-162/Disulfide bonds: #status predicted

Query Match 100.0%; Score 42; DB 1; Length 189;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTKKYSP 8  
DB 154 LTKKYSP 161  
|||||

RESULT 12  
152347  
Interferon alpha-M1 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999  
C:Accession: I52347  
R:Linnane, A.W.; Beilharz, M.W.; McMullen, G.L.; Macreadie, I.G.; Murphy, M.; Nisbet,  
Biochem. Int. 8, 725-732, 1984  
A:Title: Nucleotide sequence and expression in E. coli of a human interferon-alpha ge  
A:Reference number: I52347; MUID:84307815  
A:Accession: I52347  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-189 <RES>  
A:Cross-references: GB:M27318; NID:g184617; PIDN:AAA52726.1; PID:g306909  
C:Genetics:  
A:Gene: IFNA  
C:Superfamily: Interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 189;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTKKYSP 8  
DB 154 LTKKYSP 161  
|||||

RESULT 13  
184464  
Interferon-alpha-F - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 16-Jul-1999  
C:Accession: I84464; I37583  
R:Gren, E.Y.; Berzin, V.M.; Tsimanis, A.Y.; Apsalon, U.R.; Vishnevskii, Y.I.; Yansone  
A:Lozha, V.P.; Kavan, V.M.; Efimov, V.A.; Sverdlov, E.D.  
Dokl. Biochem. 269, 91-95, 1983  
A:Title: A new type of leukocytic interferon.  
A:Reference number: I37583  
A:Accession: I84464  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-189 <RES>  
A:Cross-references: GB:M12350; NID:g184598; PIDN:AAA52718.1; PID:g306906  
A:Accession: I37583  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-189 <RE2>  
A:Cross-references: EMBL:X00145; NID:g32724; PIDN:CAA24980.1; PID:g32725  
C:Genetics:  
A:Gene: IFNA  
C:Superfamily: Interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 189;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTKKYSP 8  
DB 154 LTKKYSP 161  
|||||

RESULT 14  
I53102  
Interferon-alpha-J1 - human  
C:Species: Homo sapiens (man)

C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999  
 C:Accession: I53102  
 R:Cohen, S.; Velan, B.; Grosfeld, H.; Shalita, Z.; Leitner, M.; Shaffer, A.  
 Dev. Biol. Stand. 60, 111-122, 1985  
 A:Title: Cloning, expression and biological activity of a new variant of human interferon  
 A:Reference number: I53102; MUID:86005847  
 A:Accession: I53102  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-189 <RES>  
 A:Cross-references: GB:M34913; NID:gl84614; PIDN:AAA36039.1; PID:gl84615  
 C:Superfamily: Interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 189;  
 Best Local Similarity 100.0%; Pred. NO. 0.28;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYS 8  
 Db 154 LTERKYS 161

RESULT 15  
 I51970  
 Interferon precursor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999  
 C:Accession: I51970  
 R:Saveliev, V.I.; Zlochevsky, M.L.; Sorokin, A.V.; Naroditskaya, V.A.; Bolotin, A.P.; De  
 Antibiot. Med. Biotechnol. 31, 592-596, 1986  
 A:Title: [Cloning and the determination of the nucleotide sequences in 2 genes of human  
 A:Reference number: I51970; MUID:87024453  
 A:Accession: I51970  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-189 <RES>  
 A:Cross-references: GB:M38289; NID:gl86407; PIDN:AAA59165.1; PID:gl86408  
 C:Genetics:  
 A:Gene: IFNA  
 C:Superfamily: Interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 189;  
 Best Local Similarity 100.0%; Pred. NO. 0.28;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYS 8  
 Db 154 LTERKYS 161

Search completed: December 13, 2001, 10:45:38  
 Job time: 58 sec

GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: December 13, 2001, 11:56:12 ; Search time 34.38 Seconds  
(without alignments)  
34.037 Million cell updates/sec

Title: US-09-424-080A-1  
Perfect score: 42  
Sequence: 1 LTKKYS P 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 287

Minimum DB seq length: 8  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

SPTREMBL17:  
1: sp.arches:  
2: sp.bacteria:  
3: sp.fungi:  
4: sp.human:  
5: sp.invertebrate:  
6: sp.mammal:  
7: sp.mhc:  
8: sp.organelle:  
9: sp.phage:  
10: sp.plant:  
11: sp.rodent:  
12: sp.virus:  
13: sp.vertebrate:  
14: sp.unclassified:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	25	59.5	8	2	Q9R9E0	Q9R9E0 bacillus su
2	14	33.3	8	8	Q9TMN4	Q9TMN4 begonia for
3	14	33.3	8	8	Q9T2Y2	Q9T2Y2 begonia tai
4	14	33.3	8	8	Q9T2Y1	Q9T2Y1 begonia apt
5	14	33.3	8	10	Q9XGL9	Q9XGL9 begonia nan
6	14	33.3	8	10	Q9XGL8	Q9XGL8 begonia chi
7	14	33.3	8	10	Q9STD5	Q9STD5 begonia pal
8	13	31.0	8	2	Q9R7T2	Q9R7T2 escherichia
9	13	31.0	8	12	Q84271	Q84271 human papil
10	12	28.6	8	6	Q9XSV1	Q9XSV1 canis fami
11	12	28.6	8	8	Q35792	Q35792 saccharomyc
12	12	28.6	8	11	Q62933	Q62933 rattus norv
13	11	26.2	8	2	Q9R5L7	Q9R5L7 clostridium
14	11	26.2	8	4	Q15895	Q15895 homo sapien
15	11	26.2	8	5	P82889	P82889 periplaneta
16	11	26.2	8	6	P82829	P82829 bos taurus
17	11	26.2	8	6	P82829	P82829 bos taurus
18	11	26.2	8	6	Q9BFA7	Q9BFA7 macroscelid
19	11	26.2	8	7	Q95213	Q95213 oryctolagus

## ALIGNMENTS

```

RESULT 1
Q9R9E0 ID Q9R9E0 PRELIMINARY; PRT; 8 AA.
AC Q9R9E0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE STAGE V SPORULATION PROTEIN E (FRAGMENT).
OS SPOVE.
GN Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID:1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:168;
RX MEDLINE:93003529; PubMed:1391053;
RA Henriques A.O., de Lencastre H., Pigot P.J.;
RT "A Bacillus subtilis morphogene cluster that includes spove is
RL homologous to the mra region of Escherichia coli.";
DR Biochimie 74:735-748(1992).
DR EMBL; X64258; CAA45556.1; -
FT NON_TER 8
SQ SEQUENCE 8 AA; 893 MW; EE75A1A33321B1A6 CRC64;

Query Match 59.5%; Score 25; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.7e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LTKKYS P 8
Db 1 MTKKTS P 8

RESULT 2
Q9TMN4 ID Q9TMN4 PRELIMINARY; PRT; 8 AA.
AC Q9TMN4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

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Q9T2Y3 begonia for  
Q4463 agrobacteri  
Q9219 neisseria m  
Q95R0 shigella dy  
Q9AGP4 arthrobacte  
Q36898 nicotiana p  
Q9S824 spinacia ol  
Q62528 mus spretus  
Q53790 streptococc  
Q45889 clostridium  
Q87471 haemophilus  
Q9R9C2 borrelia bu  
Q15901 homo sapien  
Q16468 homo sapien  
Q9Y414 homo sapien  
Q9UHK1 homo sapien  
P82618 periplaneta  
P82422 psathyrosta  
P92219 australopyr  
P92211 agropyron c  
P92215 amblyopyrum  
P92222 bromus iner  
P92227 crithopsis  
P92373 haynaldia v  
P92382 hordeum bra  
Q98YK9 human immu



GN ATPB GENE.  
 OS Begonia chitoensis.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Cucurbitales; Begoniaceae; Begonia.  
 OX NCBI\_TaxID=78254;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-16296;  
 RA Chiang I.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ007420; C845929.1; -  
 FT NON-TER 8  
 SQ SEQUENCE 8 AA; 921 MW; FA21AB01B6C775B6 CRC64;

Query Match 33.3%; Score 14; DB 10; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 4.7e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TEKK 5  
 Db 5 TETK 8

RESULT 7  
 Q9STD5 PRELIMINARY; PRT; 8 AA.  
 AC Q9STD5;  
 DT 01-MAY-2000 (TEMBLrel. 13; Created)  
 DT 01-MAY-2000 (TEMBLrel. 13; Last sequence update)  
 DT 01-MAY-2000 (TEMBLrel. 13; Last annotation update)  
 DE RIBULOSE-BISPHOSPHATE CARBOXYLASE LARGE SUBUNIT (FRAGMENT).  
 OS BECL.  
 GN Begonia palmata.  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Cucurbitales; Begoniaceae; Begonia.  
 OX NCBI\_TaxID=99386;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-16081;  
 RA Chiang I.;  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ007745; CAB53369.1; -  
 FT NON-TER 8  
 SQ SEQUENCE 8 AA; 921 MW; FA21AB01B6C775B6 CRC64;

Query Match 33.3%; Score 14; DB 10; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 4.7e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TEKK 5  
 Db 5 TETK 8

RESULT 8  
 Q9RTT2 PRELIMINARY; PRT; 8 AA.  
 AC Q9RTT2;  
 DT 01-MAY-2000 (TEMBLrel. 13; Created)  
 DT 01-MAY-2000 (TEMBLrel. 13; Last sequence update)  
 DT 01-MAY-2000 (TEMBLrel. 16; Last annotation update)  
 DE HYPOTHETICAL PROTEIN HI0004 (FRAGMENT).  
 OS YFG.  
 GN Escherichia coli.  
 OS Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-K12;  
 RX MEDLINE-97061202; PubMed-8905232;  
 RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,  
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,  
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,  
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,  
 RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
 RA Yano M., Horiuchi T.;  
 RT "A 718-kb DNA Sequence of Escherichia coli K-12 Genome Corresponding  
 RT to the 12.7-28.0 min Region on the Linkage Map."  
 RL DNA Res. 3:137-155(1996).  
 DR EMBL; D90705; BAA35310.1; -  
 FT NON-TER 1  
 SQ SEQUENCE 8 AA; 964 MW; DF133B1DD04B476A CRC64;

Query Match 31.0%; Score 13; DB 2; Length 8;  
 Best Local Similarity 40.0%; Pred. No. 4.7e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTEKK 5  
 Db 4 IAEKE 8

RESULT 9  
 Q84271 PRELIMINARY; PRT; 8 AA.  
 AC Q84271;  
 DT 01-NOV-1996 (TEMBLrel. 01; Created)  
 DT 01-NOV-1996 (TEMBLrel. 01; Last sequence update)  
 DT 01-NOV-1998 (TEMBLrel. 08; Last annotation update)  
 DE LI PROTEIN (FRAGMENT).  
 OS Human papillomavirus type 19.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=10608;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-88089511; PubMed-2826651;  
 RA Krubke J., Kraus J., Delius H., Chow L., Broker T.R., Iftner T.,  
 RA Pfister H.;  
 RT "Genetic relationship among human papillomaviruses associated with  
 RT benign and malignant tumours of patients with epidermodysplasia  
 RT verruciformis."  
 RL J. Gen. Virol. 68:3091-3103(1987).  
 DR EMBL; D00204; BAA00142.1; -  
 FT NON-TER 1  
 SQ SEQUENCE 8 AA; 987 MW; 7F432403240321A8 CRC64;

Query Match 31.0%; Score 13; DB 12; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 4.7e+05;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TEKK 5  
 Db 2 TKRK 5

RESULT 10  
 Q9XSV1 PRELIMINARY; PRT; 8 AA.  
 AC Q9XSV1;  
 DT 01-NOV-1999 (TEMBLrel. 12; Created)  
 DT 01-NOV-1999 (TEMBLrel. 12; Last sequence update)  
 DT 01-NOV-1999 (TEMBLrel. 12; Last annotation update)  
 DE RETINOBLASTOMA PROTEIN (FRAGMENT).  
 OS RBL.  
 GN Canis familiaris (Dog).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;

RN SEQUENCE FROM N.A.  
 RX MEDLINE-97049323; PubMed-8894053;  
 RA Venter P.J., Brouillette J.A., Yuzbasiyan-Gurkan V., Brewer G.J.;  
 RT "Gene-specific universal mammalian sequence-tagged sites: application  
 to the canine genome.";  
 RL Biochem. Genet. 34:321-341(1996).  
 [1]  
 RN SEQUENCE FROM N.A.  
 RA Venter P.J., Cao Y., Alexander L., Yuzbasiyan-Gurkan V.;  
 RT "Dinucleotide repeat polymorphism in the canine retinoblastoma (Rb1)  
 gene.";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF155737; AAD38807.1;  
 FT NON\_TER 1 1  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 895 MW; 1425BB18676721E3 CRC64;

Query Match 28.6%; Score 12; DB 6; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 4.7e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KYSP 8  
 I: I  
 DB 1 KHLF 4

RESULT 11  
 ID Q35792 PRELIMINARY; PRT; 8 AA.  
 AC Q35792;  
 DT 01-NOV-1996 (TEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)  
 DE 01-NOV-1998 (TEMBLrel. 08, Last annotation update)  
 DE OX13 LOCUS IN YEAST MITOCHONDRION (STRAIN D273-10B) (CODES FOR  
 CYTOCHROME OXIDASE SUBUNIT 1).  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OG Mitochondrion.  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE-81069885; PubMed-6254986;  
 RA Bonitz S.G., Coruzzi G., Thalenfeld B.E., Tzagoloff A., Macino G.;  
 RT "Assembly of the mitochondrial membrane system. Structure and  
 nucleotide sequence of the gene coding for subunit 1 of yeast  
 cytochrome oxidase.";  
 RL J. Biol. Chem. 255:11927-11941(1980).  
 DR EMBL; V00694; CAA24063.1;  
 KW Mitochondrion.  
 SQ SEQUENCE 8 AA; 1025 MW; 084693345B5AA337-CRC64;

Query Match 28.6%; Score 12; DB 8; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 4.7e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KYKS 7  
 I: I  
 DB 2 KDYN 5

RESULT 12  
 ID Q62933 PRELIMINARY; PRT; 8 AA.  
 AC Q62933;  
 DT 01-NOV-1996 (TEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)  
 DE 01-AUG-1998 (TEMBLrel. 07, Last annotation update)  
 DE HISTONE H10 (FRAGMENT).  
 OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN SEQUENCE FROM N.A.  
 RP STRAIN-WISTAR; TISSUE-TESTIS;  
 RA Khochin S., Peretti M.F., Girardot V.;  
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U49737; AAA92724.1;  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 850 MW; F4C771B5B44B01A6 CRC64;

Query Match 28.6%; Score 12; DB 11; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 4.7e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTE 3  
 I: I  
 DB 1 MTE 3

RESULT 13  
 ID Q56429 PRELIMINARY; PRT; 8 AA.  
 AC Q56429;  
 DT 01-NOV-1996 (TEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)  
 DE GAPDH (FRAGMENT).  
 OS Thermus aquaticus (subsp. thermophilus).  
 OC Bacteria; Thermus/Deinococcus group; Thermus group; Thermus.  
 OX NCBI\_TaxID=274;  
 RN SEQUENCE FROM N.A.  
 RP STRAIN-HB-8;  
 RX MEDLINE-89025722; PubMed-3052437;  
 RA Bowen D., Littlechild J.A., Fothergill J.E., Watson H.C., Hall L.;  
 RT "Nucleotide sequence of the phosphoglycerate kinase gene from the  
 extreme thermophile Thermus thermophilus. Comparison of the deduced  
 RT amino acid sequence with that of the mesophilic yeast phosphoglycerate  
 RT kinase.";  
 RL Biochem. J. 254:509-517(1988).  
 DR EMBL; X12464; CAA31005.1;  
 FT NON\_TER 1 1  
 SQ SEQUENCE 8 AA; 885 MW; 33C873333732C72B CRC64;

Query Match 26.2%; Score 11; DB 2; Length 8;  
 Best Local Similarity 60.0%; Pred. No. 4.7e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LTERK 5  
 I: I  
 DB 2 LVLKK 6

RESULT 14  
 ID Q9R5L7 PRELIMINARY; PRT; 8 AA.  
 AC Q9R5L7;  
 DT 01-MAY-2000 (TEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TEMBLrel. 14, Last annotation update)  
 DE 1,4-BETA-D-GLUCAN GLUCANOHYDROLASE (EC 3.2.1.4) (FRAGMENT).  
 OS Clostridium thermocellum.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1515;  
 RN SEQUENCE.  
 RP MEDLINE-9221850; PubMed-1567379;  
 RA Romaniec W.P., Fauth U., Kobayashi T., Huskisson N.S., Barker P.J.,



RA Demain A.L.;  
 RT "Purification and characterization of a new endoglucanase from  
 RL Clostridium thermocellum";  
 RL Biochem. J. 283:69-73(1992).  
 SQ SEQUENCE 8 AA; 823 MW; C2CIAB1DD9D1B775 CRC64;

Query Match 26.2%; Score 11; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SP 8  
 Db 1 SP 2

RESULT 15  
 Q15895 PRELIMINARY; PRT; 8 AA.  
 ID Q15895  
 AC Q15895  
 DT 01-NOV-1996 (trEMBLrel. 01, Created)  
 DT 01-NOV-1996 (trEMBLrel. 01, Last sequence update)  
 DT 01-AUG-1998 (trEMBLrel. 07, Last annotation update)  
 DE (CLONE XP6A10A) (FRAGMENT).  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PLACENTA;  
 RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,  
 RA Caskey C.T.H.;  
 RL Hum. Mol. Genet. 0:0-0(0).  
 DR EMBL; L32075; AAA73885.1;  
 FT NON\_TER 1  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 921 MW; C6C735B33686C1AA CRC64;

Query Match 26.2%; Score 11; DB 4; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 4.7e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TEKK 5  
 Db 2 TOMK 5

Search completed: December 13, 2001, 12:01:16  
 Job time: 304 sec

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; Sequence 1, Application US/09424080A
; GENERAL INFORMATION:
; APPLICANT: ZAVIALOV, Vladimir et al.
; TITLE OF INVENTION: COMPOSITION FOR ENHANCING IMMUNOSUPPRESSANTS PHARMACEUTICAL ACTI
; FILE REFERENCE: 0933-0149P
; CURRENT APPLICATION NUMBER: US/09/424,080A
; CURRENT FILING DATE: 2000-02-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A peptide corresponding to the high-affinity binding/anti-
; OTHER INFORMATION: Lymphoproliferative
; OTHER INFORMATION: Site of human IFN-alpha
US-09-424-080A-1
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; Sequence 2, Application US/09424080A
; GENERAL INFORMATION:
; APPLICANT: ZAVIALOV, Vladimir et al.
; TITLE OF INVENTION: COMPOSITION FOR ENHANCING IMMUNOSUPPRESSANTS PHARMACEUTICAL ACT
; FILE REFERENCE: 0933-0149P
; CURRENT APPLICATION NUMBER: US/09/424,080A
; CURRENT FILING DATE: 2000-02-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptides corresponding to the high-affinity binding/anti-
; OTHER INFORMATION: Lymphoproliferative
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; OTHER INFORMATION: alignment
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; LOCATION: (3)..(3)
; OTHER INFORMATION: xaa can equal E, R, D, L, I, or A
; NAME/KEY: misc.feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: xaa K, R, N, M, S, or E
; NAME/KEY: misc.feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: xaa can equal K, R, D, N, or S
; NAME/KEY: misc.feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: xaa can equal Y or H
; NAME/KEY: misc.feature
; LOCATION: (7)..(7)
; OTHER INFORMATION: xaa can equal S, R, D, N, or A
; NAME/KEY: misc.feature
; LOCATION: (8)..(8)
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US-09-424-080A-2
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Quest - Quick User-directed Expression Search Tool  
Release 5.4

-- Outline of search "iss" --

Selected search type is key against sequence data banks or files.  
Selected scope is Sequence.  
Selected sequence key from "new.key":  
new (AA) ID new AA preliminary pattern  
followed by

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OM protein - protein search, using sw model

Run on: December 13, 2001, 10:45:41 ; Search time 12.78 Seconds  
(without alignments)  
22.951 Million cell updates/sec

Title: US-09-424-080A-1  
Perfect score: 42  
Sequence: 1 LTKKYSK 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	189	1	INA1_HUMAN
2	42	100.0	189	1	INA2_HUMAN
3	42	100.0	189	1	INA3_HUMAN
4	42	100.0	189	1	INA4_HUMAN
5	42	100.0	189	1	INA5_HUMAN
6	42	100.0	189	1	INA6_HUMAN
7	36	85.7	184	1	INA7_HUMAN
8	36	85.7	184	1	INA8_HUMAN
9	36	85.7	184	1	INA9_HUMAN
10	36	85.7	184	1	INA10_HUMAN
11	36	85.7	184	1	INA11_HUMAN
12	36	85.7	184	1	INA12_HUMAN
13	36	85.7	184	1	INA13_HUMAN
14	36	85.7	184	1	INA14_HUMAN
15	35	83.3	195	1	INA15_HUMAN
16	35	83.3	195	1	INA16_HUMAN
17	34	81.0	528	1	LAD1_MOUSE
18	33	78.6	189	1	INA1_MOUSE
19	32	76.2	114	1	FVE1_MOUSE
20	31	73.8	189	1	INA1_MOUSE
21	31	73.8	189	1	INA1_MOUSE
22	31	73.8	189	1	INA2_MOUSE
23	31	73.8	189	1	INA3_MOUSE
24	31	73.8	189	1	INA4_MOUSE
25	31	73.8	189	1	INA5_MOUSE
26	31	73.8	189	1	INA6_MOUSE
27	31	73.8	189	1	INA7_MOUSE
28	31	73.8	189	1	INA8_MOUSE
29	31	73.8	189	1	INA9_MOUSE
30	31	73.8	189	1	INA10_MOUSE
31	31	73.8	189	1	INA11_MOUSE
32	30	71.4	229	1	CSEA_YEAST
33	30	71.4	270	1	TPIS_CHLMO

RESULT ID	INAL_HUMAN	STANDARD	PRT	189 AA
34	AC	P01562		
35	DT	21-JUL-1986 (Rel. 01, Created)		
36	DT	21-JUL-1986 (Rel. 01, Last sequence update)		
37	DT	20-AUG-2001 (Rel. 40, Last annotation update)		
38	DE	INTERFERON ALPHA-1/13 PRECURSOR (INTERFERON ALPHA-D) (LEIF D).		
39	GN	IFNA1 AND IFNA13.		
40	OS	Homo sapiens (Human).		
41	OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
42	OC	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.		
43	OX	NCBI_TaxID=9606;		
44	RN	SEQUENCE FROM N.A.		
45	RP	MEDLINE=81005094; PubMed=6157600;		
	RA	Mantel N., Schwarzsstein M., Streuli M., Nagata S., Muramatsu M., Weissmann C.;		
	RT	"The nucleotide sequence of a cloned human leukocyte interferon cDNA".		
	RL	Gene 10:1-10(1980).		
	RN	(2) SEQUENCE FROM N.A.		
	RP	MEDLINE=80254543; PubMed=6157095;		
	RA	Taniguchi T., Mantel N., Schwarzsstein M., Nagata S., Muramatsu M., Weissmann C.;		
	RT	"Human leukocyte and fibroblast interferons are structurally related".		
	RL	Nature 285:547-549(1980).		
	RN	(3) SEQUENCE FROM N.A.		
	RP	MEDLINE=81148795; PubMed=6163083;		
	RA	Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M., McCandless R., Seeburg P.H., Ullrich A., Yelverton E., Gray P.W.;		
	RT	"The structure of eight distinct cloned human leukocyte interferon cDNAs".		
	RL	Nature 290:20-26(1981).		
	RN	(4) SEQUENCE FROM N.A.		
	RP	MEDLINE=85003592; PubMed=6479148;		
	RA	Todokoro K., Kloussis D., Weissmann C.;		
	RT	"Two non-allelic human interferon alpha genes with identical coding regions".		
	RL	EMBO J. 3:1809-1812(1984).		
	CC	FUNCTION: PRODUCED BY MACROPHAGES. IFN-ALPHA HAVE ANTIVIRAL ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES: A PROTEIN KINASE AND AN OLIGONUCLEOTIDE SYNTHETASE.		
	CC	MISCELLANEOUS: INTERFERONS ALPHA-1 AND ALPHA-13 HAVE IDENTICAL PROTEIN SEQUENCES.		
	CC	SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA FAMILY.		
	CC	-----		
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Q57550 methanococ  
Q07788 saccharomyc  
P52891 saccharomyc  
P03160 woodchuck h  
P06275 woodchuck h  
P12898 woodchuck h  
P17396 woodchuck h  
P15402 white clove  
P78013 mycoplasma  
P05015 homo sapien  
P05000 homo sapien  
P05002 equus cabal

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CC EMBL; J00210; AAB59403.1; -  
 CC EMBL; V00537; CAA23798.1; -  
 CC EMBL; V00538; CAA23799.1; -  
 CC EMBL; X00803; CAA25381.1; -  
 CC PIR; A01826; IVHUAL  
 CC PIR; C23285; C23285.  
 CC HSSP; P01563; ZHIE.  
 CC MIM; 147578; -  
 CC MIM; 147660; -  
 CC InterPro; IPR000471; Interferon\_abd.  
 CC Pfam; PF00143; Interferon; 1.  
 CC PRINTS; PR00266; INTERFERONAB.  
 CC ProDom; PD000550; Interferon\_abd; 1.  
 CC SMART; SM00076; IFabd; 1.  
 CC PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
 CC Cytokine; Antiviral; Multigene family; Signal.  
 CC SIGNAL 1 23  
 CC CHAIN 24 189 INTERFERON ALPHA-1/13.  
 CC DISULFID 24 122 BY SIMILARITY.  
 CC DISULFID 137 162 BY SIMILARITY.  
 CC CONFLICT 137 137 A -> V (IN REF. 3).  
 CC SEQUENCE 189 AA; 21725 MW; F32F9C9B9606B69 CRC64;

Query Match 100.0%; Score 42; DB 1; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 0.24;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSYP 8  
 DB 154 LTERKYSYP 161  
 |||||

RESULT 2  
 ID IN44 HUMAN STANDARD; PRT; 189 AA.  
 AC P05014; P13158;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE INTERFERON ALPHA-4 PRECURSOR (INTERFERON ALPHA-4B) (INTERFERON  
 DE ALPHA-M1) (INTERFERON ALPHA-76).  
 GN IFNA4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86037205; PubMed=4057246;  
 RA Henco K., Brosius J., Fujisawa A., Fujisawa J.-I., Haynes J.R.,  
 RA Hochstadt J., Kovacic T., Passek M., Schamboeck A., Schmid J.,  
 RA Todokoro K., Waelchli M., Nagata S., Weissmann C.;  
 RT "Structural relationship of human interferon alpha genes and  
 RT pseudogenes.";  
 RL J. Mol. Biol. 185:227-260(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84307815; PubMed=6089830;  
 RA Linnane A.W., Bellharz M.W., McMullen G.L., Macreadie I.G.,  
 RA Murphy M., Nisbet I.T., Novitski C.E., Woodrow G.C.;  
 RT "Nucleotide sequence and expression in E. coli of a human interferon-  
 RT alpha gene selected from a genomic library using synthetic  
 RT oligonucleotides";  
 RL Biochem. Int. 8:725-732(1984).  
 CC -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL  
 CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
 CC A PROTEIN KINASE AND AN OLIGADENYLATE SYNTHETASE.  
 CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA

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CC EMBL; X02955; CAA26701.1; -  
 CC EMBL; M27216; AAA32726.1; -  
 CC PIR; E23753; IVH048.  
 CC HSSP; P01563; IITF.  
 CC MIM; 147564; -  
 CC InterPro; IPR000471; Interferon\_abd.  
 CC Pfam; PF00143; Interferon; 1.  
 CC PRINTS; PR00266; INTERFERONAB.  
 CC ProDom; PD000550; Interferon\_abd; 1.  
 CC SMART; SM00076; IFabd; 1.  
 CC PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
 CC Cytokine; Antiviral; Multigene family; Signal.  
 CC SIGNAL 1 23  
 CC CHAIN 24 189 INTERFERON ALPHA-4.  
 CC DISULFID 24 122 BY SIMILARITY.  
 CC DISULFID 52 162 BY SIMILARITY.  
 CC CONFLICT 74 74 T -> A (IN REF. 2).  
 CC CONFLICT 137 137 V -> E (IN REF. 2).  
 CC SEQUENCE 189 AA; 21808 MW; 4198F9CC8E2A880C CRC64;

Query Match 100.0%; Score 42; DB 1; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 0.24;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSYP 8  
 DB 154 LTERKYSYP 161  
 |||||

RESULT 3  
 ID IN45 HUMAN STANDARD; PRT; 189 AA.  
 AC P01563; 1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE INTERFERON ALPHA-5 PRECURSOR (INTERFERON ALPHA-G) (LEIF G) (INTERFERON  
 DE ALPHA-61).  
 GN IFNA5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86037205; PubMed=4057246;  
 RA Henco K., Brosius J., Fujisawa A., Fujisawa J.-I., Haynes J.R.,  
 RA Hochstadt J., Kovacic T., Passek M., Schamboeck A., Schmid J.,  
 RA Todokoro K., Waelchli M., Nagata S., Weissmann C.;  
 RT "Structural relationship of human interferon alpha genes and  
 RT pseudogenes.";  
 RL J. Mol. Biol. 185:227-260(1985).  
 RN [2]  
 RP SEQUENCE OF 57-189 FROM N.A.  
 RC TISSUE-Soleon;  
 RX MEDLINE=81148795; PubMed=6163083;  
 RA McCandless R., Seeburg P.H., Ulrich A., Telverton E., Gray P.W.;  
 RT "The structure of eight distinct cloned human leukocyte interferon  
 RT cDNAs.";  
 RL Nature 290:20-26(1981).  
 CC -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL

CC ACTIVITIES: INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
 CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.  
 CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.  
 CC  
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 CC  
 CC EMBL; X02956; CAA36702.1; -  
 CC PIR; A23753; IVHU16.  
 CC HSP; P01563; IITE.  
 CC MIM; I47566;  
 CC InterPro; IPR000471; Interferon\_abd.  
 CC Pfam; PF00143; Interferon; 1.  
 CC PRINTS; PR00266; INTERFERONAB.  
 CC ProDom; PD000550; Interferon\_abd; 1.  
 CC SMART; SM00076; IFabd; 1.  
 CC PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
 CC Cytokine; Antiviral; Multigene family; Signal.  
 CC SIGNAL 1 23  
 CC CHAIN 24 189 INTERFERON ALPHA-5.  
 CC DISULFID 24 122 BY SIMILARITY.  
 CC DISULFID 52 162 BY SIMILARITY.  
 CC SEQUENCE 189 AA; 21942 MW; C605992FE2E78043 CRC64;  
 CC  
 CC Query Match 100.0%; Score 42; DB 1; Length 189;  
 CC Best Local Similarity 100.0%; Pred. No. 0.24;  
 CC Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1 LTERKYP 8  
 CC | | | | | | | |  
 CC DB 154 LTERKYP 161  
 CC  
 CC RESULT 4  
 CC ID INAG HUMAN STANDARD; PRT; 189 AA.  
 CC AC P05013; 1987 (Rel. 05, Created)  
 CC DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 CC DT 13-AUG-1987 (Rel. 05, Last annotation update)  
 CC DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 CC DE INTERFERON ALPHA-6 PRECURSOR (INTERFERON ALPHA-K) (LEIF K) (INTERFERON  
 CC ALPHA-54).  
 CC GN IFNA6.  
 CC OS Homo sapiens (Human).  
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CC OX NCBI\_TaxID=9606;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RX MEDLINE=86037205; PubMed=4057246;  
 CC RA Henco K., Brosius J., Fujisawa A., Fujisawa J.-I., Haynes J.R.,  
 CC Hochstadt J., Kovacic T., Pasek M., Schamboeck A., Schmid J.,  
 CC Todokoro K., Waelchli M., Nagata S., Weissmann C.;  
 CC RT "Structural relationship of human interferon alpha genes and  
 CC pseudogenes.";  
 CC RL J. Mol. Biol. 185:227-260(1985).  
 CC  
 CC -1- FUNCTION: PRODUCED BY MACROPHAGES. IFN-ALPHA HAVE ANTIVIRAL  
 CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
 CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.  
 CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.  
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 CC  
 CC EMBL; X02956; CAA36704.1; -  
 CC PIR; A23753; IVHU16.  
 CC HSP; P01563; IITE.  
 CC MIM; I47566;  
 CC InterPro; IPR000471; Interferon\_abd.  
 CC Pfam; PF00143; Interferon; 1.  
 CC PRINTS; PR00266; INTERFERONAB.  
 CC ProDom; PD000550; Interferon\_abd; 1.  
 CC SMART; SM00076; IFabd; 1.  
 CC PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
 CC Cytokine; Antiviral; Multigene family; Signal.  
 CC SIGNAL 1 23  
 CC CHAIN 24 189 INTERFERON ALPHA-6.  
 CC DISULFID 24 122 BY SIMILARITY.  
 CC DISULFID 52 162 BY SIMILARITY.  
 CC SEQUENCE 189 AA; 22140 MW; 8C7F3F90F12C562E CRC64;  
 CC  
 CC Query Match 100.0%; Score 42; DB 1; Length 189;  
 CC Best Local Similarity 100.0%; Pred. No. 0.24;  
 CC Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1 LTERKYP 8  
 CC | | | | | | | |  
 CC DB 154 LTERKYP 161  
 CC  
 CC RESULT 5  
 CC ID INAG HUMAN STANDARD; PRT; 189 AA.  
 CC AC P01571;  
 CC DT 21-JUL-1986 (Rel. 01, Created)  
 CC DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 CC DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 CC DE INTERFERON ALPHA-17 PRECURSOR (INTERFERON ALPHA-I') (INTERFERON  
 CC ALPHA-T) (INTERFERON ALPHA-88).  
 CC GN IFNA17.  
 CC OS Homo sapiens (Human).  
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CC OX NCBI\_TaxID=9606;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RX MEDLINE=81201124; PubMed=6165082;  
 CC RA Lawn R.M., Adelman J., Dull T.J., Gross M., Goeddel D.V., Ullrich A.;  
 CC RT "DNA sequence of two closely linked human leukocyte interferon  
 CC genes.";  
 CC RL Science 212:1159-1162(1981).  
 CC RN [2]  
 CC RP SEQUENCE FROM N.A.  
 CC RX MEDLINE=85229953; PubMed=3891272;  
 CC RA Mizoguchi J., Pitha P.M., Raj N.B.K.;  
 CC RT "Efficient expression in Escherichia coli of two species of human  
 CC interferon-alpha and their hybrid molecules.";  
 CC RL DNA 4:221-232(1985).  
 CC RN [3]  
 CC RP SEQUENCE OF 14-189 FROM N.A.  
 CC RX MEDLINE=85235859; PubMed=4008999;  
 CC RA Lund B., von Gabain A., Edlund T., Ny T., Lundgren E.;  
 CC RT "Differential expression of interferon genes in a substrain of  
 CC Namalwa cells.";  
 CC RL J. Interferon Res. 5:229-238(1985).  
 CC  
 CC -1- FUNCTION: PRODUCED BY MACROPHAGES. IFN-ALPHA HAVE ANTIVIRAL  
 CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
 CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.  
 CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.

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DR EMBL; M1026; AAA52725.1; -  
 DR EMBL; V00532; CAA23793.1; -  
 DR EMBL; M71246; AAA52713.1; -  
 DR PIR; A01835; IVHUA9.  
 DR PIR; A22255; A22255.  
 DR HSSP; P01563; 1ITE.  
 DR MIM; 147583; -  
 DR InterPro; IPR000471; Interferon\_abd.  
 DR Pfam; PF00143; Interferon; 1.  
 DR PRINTS; PR00266; INTERFERONAB.  
 DR ProDom; PD000550; Interferon\_abd; 1.  
 DR SMART; SM00076; Itabd; 1.  
 DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
 KW Cytokine; Antiviral; Multigene family; Signal.  
 FT SIGNAL 1 23  
 FT CHAIN 24 189 INTERFERON ALPHA-17.  
 FT DISULFID 24 122 BY SIMILARITY.  
 FT DISULFID 52 162 BY SIMILARITY.  
 FT DISULFID 57 184 H -> P (IN REF. 1).  
 FT CONFLICT 184 184 I -> R (IN REF. 3).  
 SQ SEQUENCE 189 AA; 21728 MW; 0448EAEAB9D7FC32 CRC64;

Query Match 100.0%; Score 42; DB 1; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 0.24;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYP 8  
 |||||  
 DB 154 LTERKYP 161

RESULT 6  
 ID INAK HUMAN STANDARD; PRT; 189 AA.  
 AC P01568;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE INTERFERON ALPHA-21 PRECURSOR (INTERFERON ALPHA-F) (LEIF F).  
 GN IFNA21.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81148795; PubMed=6163083;  
 RA Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,  
 RA McCandless R., Seeburg P.H., Ullrich A., Yelverton E., Gray P.W.;  
 RT "The structure of eight distinct cloned human leukocyte interferon  
 RT cDNAs.";  
 RL Nature 290:20-26(1981).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX Gren E.Y., Berzin V.M., Tsimanis A.Y., Apsalon U.R., Vishnevskii Y.I.,  
 RA Yanson E.I.V., Dishlov A.V., Pudova N.V., Smorodintsev A.A., Lozha V.P.,  
 RA Toliev V.I., Stepanov A.N., Feldman G.Y., Meldrais Y.A., Lozha V.P.,  
 RA Kavan V.M., Efimov V.A., Sverdlov E.;  
 RT "A new type of leukocytic interferon.";  
 RL Dokl. Biochem. 269:91-95(1983).  
 CC -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL  
 CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
 CC A PROTEIN KINASE AND AN OLIGONUCLEOTIDE SYNTHETASE.  
 CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA

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DR EMBL; M12350; AAA52718.1; -  
 DR EMBL; V00540; CAA23801.1; -  
 DR EMBL; X00145; CAA24980.1; -  
 DR PIR; A01832; IVHUF.  
 DR HSSP; P01563; 2HIE.  
 DR MIM; 147584; -  
 DR InterPro; IPR000471; Interferon\_abd.  
 DR Pfam; PF00143; Interferon; 1.  
 DR PRINTS; PR00266; INTERFERONAB.  
 DR ProDom; PD000550; Interferon\_abd; 1.  
 DR SMART; SM00076; Itabd; 1.  
 DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
 KW Cytokine; Antiviral; Multigene family; Signal.  
 FT SIGNAL 1 23  
 FT CHAIN 24 189 INTERFERON ALPHA-21.  
 FT DISULFID 24 122 BY SIMILARITY.  
 FT DISULFID 52 162 BY SIMILARITY.  
 FT CONFLICT 119 119 M -> L (IN REF. 2).  
 SQ SEQUENCE 189 AA; 21759 MW; 05878D86929059B3 CRC64;

Query Match 100.0%; Score 42; DB 1; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 0.24;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYP 8  
 |||||  
 DB 154 LTERKYP 161

RESULT 7  
 ID INAL HORSE STANDARD; PRT; 184 AA.  
 AC P05003;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 01-MAR-1989 (Rel. 10, Last annotation update)  
 DE INTERFERON ALPHA-1 PRECURSOR.  
 GN Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87053170; PubMed=3022999;  
 RA Himmeler A., Hauptmann R., Adolf G.R., Swetly P.;  
 RT "Molecular cloning and expression in Escherichia coli of equine type  
 RT I interferons.";  
 RL DNA 5:345-356(1986).  
 CC -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL  
 CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
 CC A PROTEIN KINASE AND AN OLIGONUCLEOTIDE SYNTHETASE.  
 CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
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DR EMBL; M14540; AAA30953.1; -  
 DR PIR; A24912; IVHOA1.  
 DR HSSP; P01563; 2HIE.  
 DR InterPro; IPR000471; Interferon\_abd.  
 DR Pfam; PF00143; Interferon; 1.  
 DR PRINTS; PR00266; INTERFERONAB.  
 DR ProDom; PD000550; Interferon\_abd; 1.  
 DR SMART; SM00076; Ifabd; 1.  
 DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
 DR Cytokine; Antiviral; Multigene family; Signal.  
 KW SIGNAL 1 23  
 FT CHAIN 24 184 INTERFERON ALPHA-1.  
 FT DISULFID 24 122 BY SIMILARITY.  
 FT DISULFID 52 162 BY SIMILARITY.  
 SQ SEQUENCE 184 AA; 20808 MW; 9E860B8CD05C83B6 CRC64;

Query Match 85.7%; Score 36; DB 1; Length 184;  
 Best Local Similarity 87.5%; Pred. No. 3.6;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LTERKKYSP 8  
 DB 154 LOERKKYSP 161

RESULT 8  
 ID INA2\_HORSE STANDARD; PRT; 184 AA.  
 AC P05004;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 01-MAR-1989 (Rel. 10, Last annotation update)  
 DE INTERFERON ALPHA-2 PRECURSOR.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87053170; PubMed=3022999;  
 RA Hummer A., Hauptmann R., Adolf G.R., Swetly P.;  
 RT "Molecular cloning and expression in Escherichia coli of equine type  
 I interferons";  
 RL DNA 5:345-356(1986).  
 CC -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL  
 CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
 CC A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.  
 CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.  
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 CC  
 CC EMBL; M14541; AAA30950.1; -  
 CC EMBL; A15987; CAA01258.1; -  
 CC PIR; B24912; IVHOA2.  
 CC HSSP; P01563; 2HIE.  
 CC InterPro; IPR000471; Interferon\_abd.  
 CC Pfam; PF00143; Interferon; 1.  
 CC PRINTS; PR00266; INTERFERONAB.  
 CC ProDom; PD000550; Interferon\_abd; 1.  
 CC SMART; SM00076; Ifabd; 1.  
 CC PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
 CC Cytokine; Antiviral; Multigene family; Signal.  
 KW SIGNAL 1 23  
 FT CHAIN 24 184 INTERFERON ALPHA-2.  
 FT DISULFID 24 122 BY SIMILARITY.

FT DISULFID 52 162 BY SIMILARITY.  
 SQ SEQUENCE 184 AA; 20877 MW; FC15DC7D811C68EC CRC64;

Query Match 85.7%; Score 36; DB 1; Length 184;  
 Best Local Similarity 87.5%; Pred. No. 3.6;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LTERKKYSP 8  
 DB 154 LOERKKYSP 161

RESULT 9  
 ID INA3\_HORSE STANDARD; PRT; 184 AA.  
 AC P05005;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 01-MAR-1989 (Rel. 10, Last annotation update)  
 DE INTERFERON ALPHA-3 PRECURSOR.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87053170; PubMed=3022999;  
 RA Hummer A., Hauptmann R., Adolf G.R., Swetly P.;  
 RT "Molecular cloning and expression in Escherichia coli of equine type  
 I interferons";  
 RL DNA 5:345-356(1986).  
 CC -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL  
 CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
 CC A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.  
 CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.  
 CC  
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 CC  
 CC EMBL; M14542; AAA30951.1; -  
 CC EMBL; A16555; CAA01292.1; -  
 CC PIR; C24912; IVHOA3.  
 CC HSSP; P01563; 2HIE.  
 CC InterPro; IPR000471; Interferon\_abd.  
 CC Pfam; PF00143; Interferon; 1.  
 CC PRINTS; PR00266; INTERFERONAB.  
 CC ProDom; PD000550; Interferon\_abd; 1.  
 CC SMART; SM00076; Ifabd; 1.  
 CC PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
 CC Cytokine; Antiviral; Multigene family; Signal.  
 KW SIGNAL 1 23  
 FT CHAIN 24 184 INTERFERON ALPHA-3.  
 FT DISULFID 24 122 BY SIMILARITY.  
 FT DISULFID 52 162 BY SIMILARITY.  
 SQ SEQUENCE 184 AA; 20782 MW; 4C15D991ECA6D24A CRC64;

Query Match 85.7%; Score 36; DB 1; Length 184;  
 Best Local Similarity 87.5%; Pred. No. 3.6;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LTERKKYSP 8  
 DB 154 LOERKKYSP 161



```

RESULT 10
INM4_HORSE STANDARD; PRT; 184 AA.
ID INM4_HORSE
AC P05006;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE INTERFERON ALPHA-4 PRECURSOR.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE-87053170; PubMed=3022999;
RA Himmler A., Hauptmann R., Adolf G.R., Swetly P.;
RT "Molecular cloning and expression in Escherichia coli of equine type I interferons."
RL DNA 5:345-356(1986).
CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC A. PROTEIN KINASE AND AN OLIGONUCLEOTIDE SYNTHETASE.
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M14543; AAA30952.1; -
DR PIR; D24912; IVHOA4.
DR HSSP; P01563; IIFP.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; InterferonAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFab4; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Cytokine; Antiviral; Multigene family; Signal.
FT SIGNAL 1 23
FT CHAIN 24 184 INTERFERON ALPHA-4.
FT DISULFID 24 122 BY SIMILARITY.
FT DISULFID 52 162 BY SIMILARITY.
SQ SEQUENCE 184 AA; 20860 MW; FC087F46F11C68EC CRC64;

Query Match 85.7%; Score 36; DB 1; Length 184;
Best Local Similarity 87.5%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERKKYSP 8
DB 134 LQERKKYSP 161

RESULT 11
IN2A_HUMAN STANDARD; PRT; 188 AA.
ID IN2A_HUMAN
AC P01563; P01564; Q14606;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERFERON ALPHA-2 PRECURSOR (INTERFERON ALPHA-A) (LEIF A).
GN IFN2A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RX MEDLINE-81052322; PubMed=6159538;
RA Goeddel D.V., Yelverton E., Ullrich A., Heyneker H.-L., Miozzari G.,
RA Holmes W., Seeburg P.H., Dull T.J., May L., Stebbing N., Crea R.,
RA Maeda S., McCandless R., Sloma A., Tabor J.M., Gross M.,
RA Familletti P.C., Pestka S.;
RT "Human leukocyte interferon produced by E. coli is biologically
RT active."
RL Nature 287:411-416(1980).
RN [2]
SEQUENCE FROM N.A.
RP MEDLINE-81148795; PubMed=6163083;
RA Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,
RA McCandless R., Seeburg P.H., Ullrich A., Yelverton E., Gray P.M.;
RT "The structure of eight distinct cloned human leukocyte interferon
RT cDNAs."
RL Nature 290:20-26(1981).
RN [3]
SEQUENCE FROM N.A.
RP MEDLINE-8206261; PubMed=6170983;
RA Lawn R.M., Gross M., Houck C.M., Franke A.E., Gray P.V.,
RA Goeddel D.V.;
RT "DNA sequence of a major human leukocyte interferon gene."
RL Proc. Natl. Acad. Sci. U.S.A. 78:5435-5439(1981).
RN [4]
SEQUENCE FROM N.A.
RP TISSUE-BONE marrow tumor;
RX MEDLINE-86069501; PubMed=3906813;
RA Oliver G., Balbas P., Valle F., Soberon X., Bolivar F.;
RT "Cloning of human leukocyte interferon cDNA and a strategy for its
RT production in E. coli."
RL Rev. Latinoam. Microbiol. 27:141-150(1985).
RN [5]
SEQUENCE OF 7-188 FROM N.A.
RX MEDLINE-81051442; PubMed=6158094;
RA Streuli M., Nagata S., Weissmann C.;
RT "At least three human type alpha interferons: structure of alpha 2."
RL Science 209:1343-1347(1980).
RN [6]
SEQUENCE OF 24-188 FROM N.A.
RX MEDLINE-8329241; PubMed=6310510;
RA Weber H., Weissmann C.;
RT "Formation of genes coding for hybrid proteins by recombination
RT between related, cloned genes in E. coli."
RL Nucleic Acids Res. 11:5661-5669(1983).
RN [7]
SEQUENCE OF 24-112 AND 136-188.
RX MEDLINE-81052321; PubMed=6159537;
RA Allen G., Fantes K.H.;
RT "A family of structural genes for human lymphoblastoid
RT (leukocyte-type) interferon."
RL Nature 287:408-411(1980).
RN [8]
DISULFIDE BONDS.
RX MEDLINE-81123083; PubMed=6162107;
RA Wetzel R.;
RT "Assignment of the disulphide bonds of leukocyte interferon."
RL Nature 289:606-607(1981).
RN [9]
CARBOHYDRATE-LINKAGE SITE THR-129.
RX MEDLINE-91264809; PubMed=2049076;
RA Adolf G.R., Kalsner I., Ahorn H., Maurer Fogy I., Cantell K.;
RT "Natural human interferon-alpha 2 is O-glycosylated."
RL Biochem. J. 276:511-518(1991).
RN [10]
3D-STRUCTURE MODELING.
RX MEDLINE-94052087; PubMed=8234245;
RA Maggioni N.J., Windsor W.T., Hruza A., Reichert P., Tsaropoulos A.,
RA Baldwin S., Huang E., Pramanik B., Ealick S., Trotta P.P.;
RT "A homology model of human interferon alpha-2."
RL Proteins 17:62-74(1993).
RN [11]
X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RP

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RX MEDLINE-9714839; PubMed-8994971;  
 RA Radhakrishnan R., Walter L.O., Hruza A., Reichert P., Trotta P.P.,  
 RT Nagabhushan P.L., Walter M.R.;  
 FT "Zinc mediated dimer of human interferon-alpha 2b revealed by X-ray  
 RT crystallography";  
 RL Structure 4:1453-1463(1996).  
 RN [12]

RP STRUCTURE BY NMR.  
 RX MEDLINE-98118493; PubMed-9417943;  
 RA Klaus W., Gsell B., Tabhardt A.M., Wipf B., Senn H.;  
 RT "The three-dimensional high resolution structure of human interferon  
 FT alpha-2a determined by heteronuclear NMR spectroscopy in solution.";  
 RL J. Mol. Biol. 274:661-675(1997).

CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL  
 CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
 CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.

CC -1- POLYMORPHISM: TWO FORMS, ALPHA-2A AND ALPHA-2B DIFFER BY A SINGLE  
 CC RESIDUE (POSITION 46).

CC -1- PHARMACEUTICAL: AVAILABLE UNDER THE NAMES ROFERON-A (ROCHE) OR  
 CC INTRON-A (SCHERING-PLOUGH). USED AS AN ANTICANCER DRUG FOR ITS  
 CC ANTIPROLIFERATIVE ACTIVITY.

CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.

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 CC -----

CC EMBL; J00207; AAB59402.1; -  
 DR EMBL; V00544; CAA23805.1; -  
 DR EMBL; V00548; CAA23809.1; -  
 DR EMBL; V00549; CAA23810.1; -  
 DR EMBL; M54886; AAA59181.1; -  
 DR EMBL; M29883; AAA52715.1; -  
 DR EMBL; A04970; CAA00410.1; -  
 DR PIR; A01827; IVHUA3.  
 DR PIR; A01828; IVHUA2.  
 DR PDB; 2HIE; 31-AUG-94.  
 DR PDB; 1RH2; 12-NOV-97.  
 DR PDB; 1ITF; 03-DEC-97.  
 DR GlycoSuiteDB; P01563; -  
 DR MIM; 147562; -

DR InterPro; IPR000471; Interferon\_abd.

DR Pfam; PF00143; interferon; 1.

DR PRINTS; PR00266; INTERFERONAB.

DR ProDom; PD000550; Interferon\_abd; 1.

DR SMART; SM00076; IFabd; 1.

DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
 KW Cytokine; Antiviral; Multigene family; Signal; Glycoprotein;

KW Polymorphism; Pharmaceutical; 3D-structure.

FT SIGNAL 1 23

FT CHAIN 24 188 INTERFERON ALPHA-2.

FT DISULFID 24 121

FT DISULFID 52 161

FT CARBOHYD 129 129

FT O-LINKED (GALNAC. . .).

FT /FTID-CAR\_000049.

FT K -> R (IN ALPHA-2B).

FT /FTID-VAR\_004012.

FT SEQUENCE 188 AA; 21550 MW; 101DD21D394CBF97 CRC64;

Query Match 85.7%; Score 36; DB 1; Length 188;  
 Best Local Similarity 87.5%; Pred. No. 3.7;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LFEKKYSP 8

DB 153 LKEKKYSP 160

RESULT 12  
 ID INAV\_HUMAN STANDARD; PRT; 189 AA.  
 AC P01567;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE INTERFERON ALPHA-7 PRECURSOR (INTERFERON ALPHA-J1) (INTERFERON  
 DE ALPHA-J) (LEIF J).  
 OS IFNA7.  
 GN Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-86037205; PubMed-4057246;  
 RA Henco K., Brosius J., Fujisawa J.-I., Haynes J.R.,  
 RA Hochstadt J., Kovacic T., Pasek M., Schamboeck A., Schmid J.,  
 RA Todokoro K., Waelchli M., Nagata S., Weissmann C.;  
 RT "Structural relationship of human interferon alpha genes and  
 RT pseudogenes";  
 RL J. Mol. Biol. 185:227-260(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-84010248; PubMed-6181262;  
 RA Ullrich A., Gray A., Goeddel D.V., Dull T.J.;  
 RT "Nucleotide sequence of a portion of human chromosome 9 containing a  
 RT leukocyte interferon gene cluster.";

CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL  
 CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:  
 CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.

CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.

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 CC -----

CC EMBL; V00531; CAA23792.1; -

CC EMBL; X02960; CAA26706.1; -

CC PIR; A01831; IVHUA0.

CC HSSP; P01563; 2HIE.

CC MIM; 147567; -

DR InterPro; IPR000471; Interferon\_abd.

DR Pfam; PF00143; interferon; 1.

DR PRINTS; PR00266; INTERFERONAB.

DR ProDom; PD000550; Interferon\_abd; 1.

DR SMART; SM00076; IFabd; 1.

DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.

KW Cytokine; Antiviral; Multigene family; Signal.

FT SIGNAL 1 23

FT CHAIN 24 189 INTERFERON ALPHA-7.

FT DISULFID 24 122 BY SIMILARITY.

FT DISULFID 52 162 BY SIMILARITY.

FT SEQUENCE 189 AA; 22106 MW; 90DF6F5C81E339A42 CRC64;

```

RESULT 13
INAD_HUMAN STANDARD; PRT; 189 AA.
AC P01570;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE (INTERFERON ALPHA-14 PRECURSOR (INTERFERON ALPHA-H) (LEIF, H)
DE (INTERFERON LAMBDA-2-H)
GN IFNA14.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=86037205; PubMed=4057246;
RA Henco K., Brosius J., Fujisawa J.-I., Haynes J.R.,
RA Hochstadt J., Kovacic T., Pasak M., Schamboeck A., Schmid J.,
RA Todokoro K., Waelchli M., Nagata S., Weissmann C.;
RT "Structural relationship of human interferon alpha genes and
RT pseudogenes.";
RL J. Mol. Biol. 185:227-260(1985).
RN [2]
RP MEDLINE=81201124; PubMed=6165082;
RA Lawn R.M., Adelman J., Dull T.J., Gross M., Goeddel D.V., Ullrich A.;
RT "DNA sequence of two closely linked human leukocyte interferon
RT genes.";
RL Science 212:1159-1162(1981).
RN [3]
RP MEDLINE=81148795; PubMed=6163083;
RA Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,
RA McCandless R., Seeburg P.H., Ullrich A., Vervort E., Gray P.W.;
RT "The structure of eight distinct cloned human leukocyte interferon
RT cDNAs.";
RL Nature 290:20-26(1981).
CC -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.
CC -!- MISCELLANEOUS: A VARIANT SEQUENCE DIFFERS IN 3 POSITIONS. THE LAST
CC 2 BEING THE RESULT OF A DELETION FOLLOWED BY AN INSERTION.
CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
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CC -----
DR EMBL: V00533; CAA33794.1;
DR EMBL: X02959; CAA36705.1;
DR EMBL: Y00542; CAA3803.1;
DR PIR: C23753; IVHU14.
DR HSP: P01563; 2HIE.
DR NIM: 147579;
DR InterPro: IPR000471; Interferon_abd.
DR Pfam: PF00143; Interferon; 1.
DR PRINTS: PR00266; INTERFERONAB.
DR ProDom: PD000550; Interferon_abd; 1.
DR SMART: SM00076; IFabid; 1.
DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
DR Cytokine; Antiviral; Multigene family; Glycoprotein; Signal.
KW SIGNAL
FT CHAIN 1 23
FT CHAIN 24 189 INTERFERON ALPHA-14.
FT DISULFID 24 122 BY SIMILARITY.
FT DISULFID 52 162 BY SIMILARITY.
FT CARBOHYD 25 175 N-LINKED (GLCNAC... ) (POTENTIAL).
FT VARIANT 175 175 L -> F.

FT VARIANT 182 182 /FTID-VAR_004013.
FT VARIANT 184 184 Q->K.
FT VARIANT 184 184 /FTID-VAR_004014.
FT SEQUENCE 189 AA; 22062 MW; 86B71E2FD644FE7 CRC64;
SQ
Query Match 85.7%; Score 36; DB 1; Length 189;
Best Local Similarity 87.5%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LTERKYSKSP 8
DB 154 LMERKYSKSP 161
RESULT 14
INA_FELCA STANDARD; PRT; 194 AA.
AC P35849; Q28831;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERFERON ALPHA PRECURSOR (IFN-ALPHA).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP MEDLINE=93233151; PubMed=1377975;
RA Nakamura N., Sudo T., Matsuda S., Yanai A.;
RT "Molecular cloning of feline interferon cDNA by direct expression.";
RL Biosci. Biotechnol. Biochem. 56:211-214(1992).
RN [2]
RP MEDLINE=93291253; PubMed=7685640;
RA Ueda Y., Sakurai T., Yanai A.;
RT "Homogeneous production of feline interferon in silkworm by replacing
RT single amino acid code in signal peptide region in recombinant
RT baculovirus and characterization of the product.";
RL J. Vet. Med. Sci. 55:251-258(1993).
CC -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.
CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
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CC -----
DR EMBL: S62636; BAB37160.2;
DR EMBL: J50664; J50664.
DR HSP: P01563; 2HIE.
DR InterPro: IPR000471; Interferon_abd.
DR Pfam: PF00143; Interferon; 1.
DR PRINTS: PR00266; INTERFERONAB.
DR ProDom: PD000550; Interferon_abd; 1.
DR SMART: SM00076; IFabid; 1.
DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
DR Cytokine; Antiviral; Signal.
KW SIGNAL
FT CHAIN 1 23
FT CHAIN 24 194 INTERFERON ALPHA.
FT DISULFID 24 123 BY SIMILARITY.
FT DISULFID 52 166 BY SIMILARITY.
FT CARBOHYD 102 102 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CONFLICT 21 21 S -> V (IN REF. 2).

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SO SEQUENCE 194 AA; 21892 MW; D10E916E3755BFEF CRC64;

Query Match 85.7%; Score 36; DB 1; Length 194;  
Best Local Similarity 87.5%; Pred. No. 3.8;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERKYS 8

DB 158 LOERKYS 165

RESULT 15

INAB\_HUMAN

ID INAB\_HUMAN STANDARD; PRT; 189 AA.

AC P32881; P09236; P01565;

DT 21-JUL-1986 (Rel. 01, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE INTERFERON ALPHA-8 PRECURSOR (INTERFERON ALPHA-B2) (INTERFERON

DE ALPHA-B) (LEIF B).

GN IFNA8

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=86037205; PubMed=4057246;

RA Henco K., Brosius J., Fujisawa J., Haynes J.R.,

RA Hochstadt J., Kovacic T., Pasek M., Schamboeck A., Schmid J.,

RA Todokoro K., Waelchli M., Nagata S., Weissmann C.;

RT "Structural relationship of human interferon alpha genes and

RT pseudogenes.";

RL J. Mol. Biol. 185:227-260(1985).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=84183614; PubMed=6325303;

RA Bowden D.W., Mao J., Gill T., Hsiao K., Lillquist J.S., Testa D.,

RA Vovis G.F.;

RT "Cloning of eukaryotic genes in single-strand phage vectors: the

RT human interferon genes.";

RL Gene 27:87-99(1984).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=81174733; PubMed=6164048;

RA Yelvertown E., Leung D.W., Weck P., Gray P.W., Goeddel D.V.;

RT "Bacterial synthesis of a novel human leukocyte interferon.";

RL Nucleic Acids Res. 9:731-741(1981).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=81148795; PubMed=6163083;

RA Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,

RA McCandless R., Seeburg P.H., Ullrich A., Yelvertown E., Gray P.W.;

RT "The structure of eight distinct cloned human leukocyte interferon

RT cDNAs.";

RL Nature 290:20-26(1981).

CC CC

CC -1- FUNCTION: PRODUCED BY MACROPHAGES. IFN-ALPHA HAVE ANTIVIRAL

CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:

CC A PROTEIN KINASE AND AN OLIGONUCLEOTIDE SYNTHETASE.

CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA

CC FAMILY.

CC CC

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CC -----

CC EMBL; V00545; CAA23806.1; -

CC EMBL; K01900; AAA52716.1; -

DR EMBL; X03125; CAA26903.1; -  
DR EMBL; V00550; CAA23811.1; -  
DR PIR; D23753; IVHU18.  
DR PIR; A01829; IVHDA4.  
DR HSSP; P01563; 2HIE.  
DR MIM; 147568; -  
DR InterPro; IPR000471; Interferon\_abd.  
DR Pfam; PF00143; interferon; 1.  
DR PRINTS; PR00266; INTERFERONAB.  
DR ProDom; PD000550; Interferon\_abd; 1.  
DR SMART; SM00076; IFabd; 1.  
DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
KW Cytokine; Antiviral; Multigene family; Signal.  
FT SIGNAL 1 23  
FT CHAIN 24 189 INTERFERON ALPHA-8.  
FT DISULFID 24 122 BY SIMILARITY.  
FT DISULFID 52 162 BY SIMILARITY.  
FT CONFLICT 8 8 L -> M (IN REF. 3 AND 4).  
FT CONFLICT 121 124 SCVM -> VLCD (IN REF. 3 AND 4).  
SQ SEQUENCE 189 AA; 21989 MW; 83128DA2B6DBBZCI CRC64;

Query Match 83.3%; Score 35; DB 1; Length 189;  
Best Local Similarity 100.0%; Pred. No. 5.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYS 7

DB 154 LTERKYS 160

Search completed: December 13, 2001, 10:50:49  
Job time: 308 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 13, 2001, 10:45:11 ; Search time 35.74 Seconds  
(without alignments)  
32.741 Million cell updates/sec

Title: US-09-424-080A-1  
Perfect score: 42  
Sequence: 1 LTERKYSK 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_unclassified:\*
- 14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	166	4 Q9UMJ3	Q9umj3 homo sapien
2	42	100.0	181	4 Q14608	Q14608 homo sapien
3	42	100.0	189	4 Q14605	Q14605 homo sapien
4	42	100.0	189	4 Q14639	Q14639 homo sapien
5	42	100.0	189	4 Q14607	Q14607 homo sapien
6	36	85.7	108	6 Q9N1U6	Q9nlu6 equus caball
7	36	85.7	170	6 Q29114	Q29114 sus scrofa
8	36	85.7	170	6 Q29115	Q29115 sus scrofa
9	36	85.7	730	10 Q9S9M5	Q9s9m5 arabidopsis
10	34	81.0	181	3 Q13619	Q13619 schizosacch
11	34	81.0	577	5 Q358Y5	Q358y5 schizosacch
12	34	81.0	1154	5 Q9V6S9	Q9v6s9 drosophila
13	33	78.6	110	10 Q9S1R5	Q9s1r5 arabidopsis
14	33	78.6	334	2 Q9CKR2	Q9ckr2 pasteurella
15	33	78.6	767	11 Q9WU7	Q9wtu7 mus musculus
16	32	76.2	83	5 Q9V8W6	Q9v8w6 drosophila
17	32	76.2	400	5 Q9V8Y9	Q9v8y9 drosophila
18	32	76.2	414	10 Q9SX74	Q9sx74 arabidopsis
19	32	76.2	573	5 Q23323	Q23323 caenorhabdi

20	32	76.2	1528	5	Q95022	Q95022 cryptospori
21	31	73.8	60	12	Q91E09	Q91e09 cotton leaf
22	31	73.8	113	2	Q9F554	Q9f554 escherichia
23	31	73.8	118	12	Q88551	Q88551 tomato yell
24	31	73.8	118	12	Q73583	Q73583 cotton leaf
25	31	73.8	118	12	Q9QDE8	Q9qde8 tomato leaf
26	31	73.8	118	12	Q9IGY3	Q9igy3 tobacco leaf
27	31	73.8	118	12	Q9IGX7	Q9igx7 tobacco gem
28	31	73.8	118	12	Q9GDR5	Q9gdr5 chilli leaf
29	31	73.8	136	11	Q61717	Q61717 mus musculu
30	31	73.8	176	11	Q9D380	Q9d380 mus musculu
31	31	73.8	190	11	Q61716	Q61716 mus musculu
32	31	73.8	190	11	Q61718	Q61718 mus musculu
33	31	73.8	190	11	Q61719	Q61719 mus musculu
34	31	73.8	197	2	Q06983	Q06983 bacillus su
35	31	73.8	199	4	Q9X698	Q9x698 homo sapien
36	31	73.8	201	2	Q45137	Q45137 bacteroides
37	31	73.8	239	2	Q524D2	Q524d2 escherichia
38	31	73.8	261	2	Q96679	Q96679 bacillus su
39	31	73.8	275	2	Q94124	Q94124 acinetobact
40	31	73.8	285	3	Q00875	Q00875 fusarium so
41	31	73.8	322	4	Q92780	Q92780 homo sapien
42	31	73.8	401	1	Q59114	Q59114 pyrococcus
43	31	73.8	439	2	Q9RGV4	Q9rgv4 salmonella
44	31	73.8	510	2	Q9RK66	Q9rk66 streptomyce
45	31	73.8	589	2	Q9RMV4	Q9rmv4 bacillus an

## ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	166 AA.
Q9UMJ3				
ID	Q9UMJ3			
AC	Q9UMJ3			
DT	01-MAY-2000 (T-EMBLrel. 13, Created)			
DT	01-MAY-2000 (T-EMBLrel. 13, Last sequence update)			
DT	01-JUN-2001 (T-EMBLrel. 17, Last annotation update)			
DE	IFNA PROTEIN (FRAGMENT)			
GN	IFNA			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-8329241; PubMed-6310510;			
RA	Weber H., Weissmann C.;			
RT	*Formation of genes coding for hybrid proteins by recombination			
RT	between related, cloned genes in E. coli.*;			
RL	Nucleic Acids Res. 11:5661-5669(1983).			
CC	-!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA			
CC	FAMILY.			
DR	EMBL; M29884; AAA52714.1; .			
DR	HSSP; P01563; 2HIE.			
DR	InterPro; IPR000471; Interferon_abd.			
DR	Pfam; PF00143; Interferon; 1.			
DR	PRINTS; PR00266; INTERFERONAB.			
DR	ProDom; PD000550; Interferon_abd; 1.			
DR	SMART; SM00076; IFabd; 1.			
DR	PROSITE; PS00252; INTERFERON_A_B_D; 1.			
KW	Antiviral; Cytokine.			
FT	NON_TER			
SQ	SEQUENCE 166 AA; 19386 MW; 4152EA2A78361BB8 CRC64;			

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.65;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSK 8  
DB 131 LTERKYSK 138

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RESULT 2
Q14608 ID Q14608 PRELIMINARY; PRT; 181 AA.
AC Q14608;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE LEUCOCYTE INTERFERON-ALPHA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8505623; PubMed=6548765;
RA Gren E., Berzin V.M., Jansone I., Tsimanis A., Vishnevsky Y.,
RA Adaslong U.; leukocyte interferon subtype and structural comparison of
RT alpha interferon genes.;
RL J. Interferon Res. 4:609-617(1984).
CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
DR EMBL; M28586; AAA36041.1; -.
DR HSSP; P01563; 2HIE.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine; Signal.
SQ SEQUENCE 181 AA; 20878 MW; 3DB45120764EBABC CRC64;

Query Match 100.0%; Score 42; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.71; 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

QY 1 LTEKKYSP 8
DB 146 LTEKKYSP 153

RESULT 3
Q14605 ID Q14605 PRELIMINARY; PRT; 189 AA.
AC Q14605;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE INTERFERON-ALPHA 13 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86037205; PubMed=4057246;
RA Henco K., Brosius J., Fujisawa A., Fujisawa J.I., Haynes J.R.,
RA Hochstadt J., Kovacic T., Pasek M., Schamboeck A., Schmid J.,
RA Todokoro K., Waelchli M., Nagata S., Weissmann C.;
RT "Structural relationship of human interferon alpha genes and
pseudogenes.";
RL J. Mol. Biol. 185:227-260(1985).
CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
DR EMBL; X75934; CAA53538.1; -.

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DR EMBL; A07163; CAA00632.1; -.
DR HSSP; P01563; 2HIE.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 189 POTENTIAL.
SQ SEQUENCE 189 AA; 21697 MW; 442F8BB754D88398 CRC64;

Query Match 100.0%; Score 42; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 0.74; 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

QY 1 LTEKKYSP 8
DB 154 LTEKKYSP 161

RESULT 4
Q14639 ID Q14639 PRELIMINARY; PRT; 189 AA.
AC Q14639;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE LEUCOCYTE INTERFERON PRECURSOR.
OS IFNA.
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87024453; PubMed=3767336;
RA Savoliev V.I., Zlochevsky M.L., Sorokin A.V., Naroditskaya V.A.,
RA Bolotin A.P., Demvanova N.G., Kozlov Y.I., Neznanov N.S.,
RA Gazaryan K.G., Monastyrskaya G.S., Sverdlov E.D.;
RT "Cloning and the determination of the nucleotide sequences in 2 genes
of human leukocyte interferons";
RL Antibiog. Med. Biotechnol. 31:592-596(1986).
CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
DR EMBL; M38289; AAA59165.1; -.
DR HSSP; P01563; 2HIE.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 189 POTENTIAL.
SQ SEQUENCE 189 AA; 21781 MW; 9D6E31870F1A88A1 CRC64;

Query Match 100.0%; Score 42; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 0.74; 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

QY 1 LTEKKYSP 8
DB 154 LTEKKYSP 161

RESULT 5
Q14607 ID Q14607 PRELIMINARY; PRT; 189 AA.

```

AC Q14607;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE INTERFERON-ALPHA-J1 (IFN-ALPHA-J1).  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86005847; PubMed=2995168;  
 RA Cohen S., Vellan B., Grosfeld H., Shalita Z., Leitner M.,  
 RA Shaffer A.;  
 RT Cloning, expression and biological activity of a new variant of human  
 RT Interferon alpha identified in virus induced lymphoblastoid cells.;  
 RL Dev. Biol. 60:111-122(1985).  
 CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.  
 CC EMBL; M34913; AAA36039.1; .  
 DR HSP; P01563; 2HIE.  
 DR InterPro; IPR000471; Interferon\_abd.  
 DR Pfam; PF00143; Interferon; 1.  
 DR PRINTS; PR00266; INTERFERONAB.  
 DR ProDom; PD000550; Interferon\_abd; 1.  
 DR SMART; SM00076; IFabd; 1.  
 DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
 KW Antiviral; Cytokine.  
 SQ SEQUENCE 189 AA; 22048 MW; 2AF6F48447BB72B3 CRC64;

Query Match 100.08; Score 42; DB 4; Length 189;  
 Best Local Similarity 100.08; Pred. No. 0.74;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTERKYS 8  
 DB 154 LTERKYS 161

RESULT 6  
 ID Q9N1U6 PRELIMINARY; PRT; 108 AA.  
 AC Q9N1U6;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE INTERFERON ALPHA-1 (FRAGMENT).  
 GN IFN1A.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20082971; PubMed=10613847;  
 RA Caetano A.R., Shlue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,  
 RA Bowling A.T., Murray J.D.;  
 RT A comparative gene map of the horse (Equus caballus).;  
 RL Genome Res. 9:1239-1249(1999).  
 CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.  
 CC EMBL; AF135017; AAF29603.1; .  
 DR InterPro; IPR000471; Interferon\_abd.  
 DR Pfam; PF00143; Interferon; 1.  
 DR PRINTS; PR00266; INTERFERONAB.  
 DR ProDom; PD000550; Interferon\_abd; 1.  
 DR SMART; SM00076; IFabd; 1.  
 DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
 KW Antiviral; Cytokine.  
 DR NON\_TER 1  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 12420 MW; 028CA54FFA97F4CD CRC64;

Query Match 85.7%; Score 36; DB 6; Length 108;  
 Best Local Similarity 87.5%; Pred. No. 7.1;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LTERKYS 8  
 DB 95 LTERKYS 102

RESULT 7  
 ID Q29114 PRELIMINARY; PRT; 170 AA.  
 AC Q29114;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE SHORT TYPE I INTERFERON PRECURSOR.  
 GN SPI IFN.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE-WHOLE CONCEPTUS (EMBRYO PLUS TROPHOBLAST);  
 RX MEDLINE=93374975; PubMed=7690039;  
 RA Lefevre F., Boulay V.;  
 RT A novel and atypical type one interferon gene expressed by  
 RT trophoblast during early pregnancy.;  
 RL J. Biol. Chem. 268:19760-19768(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-WHOLE CONCEPTUS (EMBRYO PLUS TROPHOBLAST);  
 RX MEDLINE=86232600; PubMed=3714490;  
 RA von Heijne G.;  
 RT A new method for predicting signal sequence cleavage sites.;  
 RL Nucleic Acids Res. 14:4683-4690(1986).  
 CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 CC FAMILY.  
 CC EMBL; 222706; CAA80407.1; .  
 DR HSP; P01563; 1TFF.  
 DR InterPro; IPR000471; Interferon\_abd.  
 DR Pfam; PF00143; Interferon; 1.  
 DR PRINTS; PR00266; INTERFERONAB.  
 DR ProDom; PD000550; Interferon\_abd; 1.  
 DR SMART; SM00076; IFabd; 1.  
 DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
 KW Antiviral; Cytokine; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 170 SHORT TYPE I INTERFERON.  
 FT VARIANT 88 88 S -> G.  
 FT VARIANT 101 101 N -> T.  
 SQ SEQUENCE 170 AA; 19906 MW; FED195EAFDD99AAB CRC64;

Query Match 85.7%; Score 36; DB 6; Length 170;  
 Best Local Similarity 87.5%; Pred. No. 11;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LTERKYS 8  
 DB 146 LTERKYS 153

RESULT 8  
 ID Q29115 PRELIMINARY; PRT; 170 AA.  
 AC Q29115;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE SHORT TYPE I INTERFERON PRECURSOR.  
 GN SPI IFN.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=LARGE WHITE BREED; TISSUE=LIVER;  
 RX MEDLINE=86232600; PubMed=3714490;  
 RA von Heijne G.;  
 RT "A new method for predicting signal sequence cleavage sites.";  
 RL Nucleic Acids Res. 14:4683-4690(1986).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=LARGE WHITE BREED; TISSUE=LIVER;  
 RX MEDLINE=87174805; PubMed=3550702;  
 RA Singer D.S., Parent L.J., Ehrlich R.;  
 RT "Identification and DNA sequence of an interspersed repetitive DNA  
 element in the genome of the miniature swine.";  
 RL Nucleic Acids Res. 15:2780-2780(1987).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=LARGE WHITE BREED; TISSUE=LIVER;  
 RX MEDLINE=93374975; PubMed=7690039;  
 RA Lefevre F., Boulay V.;  
 RT "A novel and atypical type one interferon gene expressed by  
 trophoblast during early pregnancy.";  
 RL J. Biol. Chem. 268:19760-19768(1993).  
 CC -I- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
 FAMILY.  
 DR EMBL: 222707; CAA80408.1; -.  
 DR HSSP: P01563; LITF.  
 DR InterPro: IPR000471; Interferon\_abd.  
 DR Pfam: PF00143; Interferon\_1.  
 DR PRINTS: PR00266; INTERFERONAB.  
 DR ProDom: PD000550; Interferon\_abd. 1.  
 DR SMART: SM00076; IFabd. 1.  
 DR PROSITE: PS00252; INTERFERON\_A\_B\_D; 1.  
 DR Antiviral; Cytokine; Signal.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 170 SHORT TYPE I INTERFERON.  
 SQ SEQUENCE 170 AA; 19863 MW; 563F7D2AE716AF51 CRC64;

Query Match 85.7%; Score 36; DB 6; Length 170;  
 Best Local Similarity 87.5%; Pred. No. 11;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERKYSYP 8  
 Db 146 LTERKYSYP 153

RESULT 9  
 Q9S9M5 PRELIMINARY; PRT; 730 AA.  
 AC Q9S9M5  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE T24D18.20 PROTEIN.  
 GN T24D18.20.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RA Liu S.X., Yu G., Sakano H., Jhaveri A., Lee J.M., Lenz C., Pham P.,  
 RA Toriumi M., Chin C., Chiou J., Choi E., Chung M., Gonzalez A.,

RA Howing B., Koo T., Li J., Liu A., Vaysberg M., Altafi H., Brooks S.,  
 RA Buehler E., Chao Q., Conn L., Conway A., Hansen N., Johnson-Hopson C.,  
 RA Khan S., Kim C., Lam B., Nguyen M., Palm C., Shinn P., Tambunga G.,  
 RA Davis R.W., Ecker J.R., Federpiel N.A., Theologis A.;  
 RT "The sequence of BAC T24D18 from Arabidopsis thaliana chromosome 1.";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RA Theologis A.;  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RA Theologis;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 CC -I- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL: AC010924; AF18507.1;  
 DR InterPro: IPR000719; Euk\_Pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_kin\_actsite.  
 DR Pfam: PF00069; Pkinase; 1.  
 DR SMART: SM00221; STYK; 1.  
 DR PROSITE: PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR KW ATP-binding; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 730 AA; 81210 MW; B51DB48D999C73B5 CRC64;

Query Match 85.7%; Score 36; DB 10; Length 730;  
 Best Local Similarity 75.0%; Pred. No. 45;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSYP 8  
 Db 224 LTERKYSYP 231

RESULT 10  
 ID 013619 PRELIMINARY; PRT; 181 AA.  
 AC 013619  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE P1028 PROTEIN (HYPOTHETICAL 20.3 KDA PROTEIN).  
 GN P1028 OR SPBP2H7.03  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=972 H-;  
 RA Kushida N., Yamazaki S., Tanaka T., Jinno K., Haikawa Y., Yamazaki J.,  
 RA Yamamoto S., Sekine M., Oguchi A., Nagai Y., Sakai M., Aoki K.,  
 RA Ogura K., Otsuka R., Kudo Y., Yanagida M., Machida M., Zhang M.Q.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=972H-;  
 RA Murphy L., Harris D., Wood V., Rajandream M.A., Barrell B.G.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB004535; BAA21407.1; -.  
 DR EMBL: AL590883; CAC37371.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 181 AA; 20293 MW; 2D6A1B61F0FD51E8 CRC64;

Query Match 81.0%; Score 34; DB 3; Length 181;  
 Best Local Similarity 85.7%; Pred. No. 30;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



QY 2 TEKLYSP 8  
:|||||  
Db 70 SEKLYSP 76

RESULT 11

Q3595 PRELIMINARY; PRT; 577 AA.  
AC 01-JAN-1998 (TEMBLrel. 05, Created)  
DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)  
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)  
DE MYOCHONDRIAL HSP70 HOMOLOG.  
OS Vairimorpha neatrix.  
OC Eukaryota; Microsporidia; Burenellidae; Vairimorpha.  
OX NCBI\_TaxID=6039;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-SPORES;  
RA Hirt R.P., Healy B., Vossbrinck C.R., Canning E.U., Embley T.M.;  
RL Curr. Biol. 7:0-0(1997).  
DR EMBL: AF008215; AAB81494.1; -  
DR InterPro: IPR001023; HSP70.  
DR Pfam: PF00012; HSP70; 1.  
DR PROSITE: PS00297; HSP70.1; 1.  
DR PROSITE: PS00329; HSP70.2; 1.  
SQ SEQUENCE 577 AA; 64744 MW; C649B069A94D0D8B CRC64;

Query Match 81.0%; Score 34; DB 5; Length 577;  
Best Local Similarity 75.0%; Pred. No. 91;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTKLYSP 8  
:|||||  
Db 110 IDEKLYSP 117

RESULT 12

Q3V6S9 PRELIMINARY; PRT; 1154 AA.  
AC Q9V6S9;  
DT 01-MAY-2000 (TEMBLrel. 13, Created)  
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TEMBLrel. 13, Last annotation update)  
DE CG18368 PROTEIN.  
GN CG18368.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BERKELEY;  
EX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Stanton R.C., Rogers Y.-H.C., Blazef R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablo K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195(2000).  
DR EMBL: AE003817; AAF58343.1; -  
DR FlyBase: FBgn0033864; CG18368.  
SQ SEQUENCE 1154 AA; 134414 MW; A1985DEF780A01BA CRC64;

Query Match 81.0%; Score 34; DB 5; Length 1154;  
Best Local Similarity 85.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TEKLYSP 8  
:|||||  
Db 166 TKKLYSP 172

RESULT 13

Q9SY5 PRELIMINARY; PRT; 110 AA.  
AC Q9SY5;  
DT 01-MAY-2000 (TEMBLrel. 13, Created)  
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)  
DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)  
DE HYPOTHETICAL 13.2 KDA PROTEIN.  
GN C7A10.800 OR AT4G36560.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bevan M., Terry N., Vos P., Heljnen L., Mewes H.W., Mayer K.F.X.,  
RA Schueller C.;  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: Z99708; CAB16837.1; -  
DR EMBL: AL161589; CAB80322.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 110 AA; 13189 MW; 82DA67BF97311BA8 CRC64;

Query Match 78.6%; Score 33; DB 10; Length 110;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EKKLYSP 8

Db 36 EKKYSP 41  
|||||

## RESULT 14

Q9WU7 PRELIMINARY; PRT; 334 AA.  
AC Q9WU7; 01-JUN-2001 (TRENBLrel. 17, Created)  
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
DE HPAA.  
GN HPAA OR PM1524.  
OS Pasteurella multocida.  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
OC Pasteurella.  
OX NCBI\_TaxID=747;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PM70;  
RX MEDLINE=21145866; PubMed=11248100;  
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;  
RT "Complete genomic sequence of Pasteurella multocida Pm70.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).  
CC -1- SIMILARITY: BELONGS TO THE ARAC/XVLS FAMILY OF TRANSCRIPTIONAL  
REGULATORS.  
DR EMBL: AF006189; AAK03608.1; -  
DR InterPro: IPR000005; HTHARAC.  
DR Pfam: PF00165; HTH\_ARAC; 1.  
DR PRINTS: PR00032; HTHARAC.  
DR SMART: SM00342; HTH\_ARAC; 1.  
DR PROSITE: PS00041; HTH\_ARAC\_FAMILY\_1; UNKNOWN\_1.  
DR PROSITE: PS0124; HTH\_ARAC\_FAMILY\_2; 1.  
KW Complete proteome; DNA-binding; Transcription regulation.  
SQ SEQUENCE 334 AA; 39714 MW; 8532929C52246503 CRC64;

Query Match 78.6%; Score 33; DB 2; Length 334;

Best Local Similarity 100.0%; Pred. No. 85;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EKKYSP 8  
|||||  
DB 214 EKKYSP 219

## RESULT 15

Q9WU7 PRELIMINARY; PRT; 767 AA.  
AC Q9WU7;  
DT 01-NOV-1999 (TRENBLrel. 12, Created)  
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)  
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
DE APOPTOSIS-LINKED PROTEIN 4, DELTAC FORM (FRAGMENT).  
GN PDCD11 OR ALG-4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99244237; PubMed=10229231;  
RA Lacana' E., D'Adamo L.;  
RT "Regulation of fas ligand expression and cell death by apoptosis-  
linked gene 4.";  
RL Nat. Med. 5:542-547(1999).  
DR EMBL: AF055668; AAD20941.1; -  
DR HSSP: P05055; LSRO.  
DR MGD: MGI:1341788; Pdc11.  
DR InterPro: IPR000110; Ribosomal\_S1.  
DR InterPro: IPR003029; S1.  
DR Pfam: PF00575; S1; 4.  
DR PRINTS: PR00681; RIBOSOMALS1.

DR SMART: SM00316; S1; 6.  
FT NON\_TER 1  
FT NON\_TER 767 767  
SQ SEQUENCE 767 AA; 84512 MW; 81B692B073E697FA CRC64;

Query Match 78.6%; Score 33; DB 11; Length 767;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EKKYSP 8  
|||||  
DB 101 EKKYSP 106

Search completed: December 13, 2001, 10:50:30  
Job time: 319 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 13, 2001, 10:44:40 ; Search time 38.61 Seconds  
(without alignments)  
13.348 Million cell updates/sec

Title: US-09-424-080A-1  
Perfect score: 42  
Sequence: 1 LTKKYSP 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq.ll01.\*  
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2: /SIDSB/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
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21: /SIDSB/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SIDSB/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	100.0	11	15 AAR47561	Interferon-recepto
2	42	100.0	18	15 AAR47562	Interferon-recepto
3	42	100.0	90	21 AAY55987	Partial human inte
4	42	100.0	133	3 AAP20109	Sequence encoded b
5	42	100.0	150	12 AAR11799	Interference alpha 8
6	42	100.0	162	6 AAP50168	Sequence of hybrid
7	42	100.0	165	4 AAP30687	Thr14, Met16 mutan
8	42	100.0	165	18 AAW43382	Human interferon-a
9	42	100.0	165	18 AAW43386	Human interferon-a
10	42	100.0	165	18 AAW43387	Human interferon-a
11	42	100.0	165	18 AAW43390	Human interferon-a

12	42	100.0	165	20 AAY43492	A human interferon
13	42	100.0	165	21 AAY82887	N-terminal modifie
14	42	100.0	165	21 AAY44828	Hybrid interferon
15	42	100.0	165	21 AAY44876	Human hybrid inter
16	42	100.0	165	4 AAF30863	Synthetic human le
17	42	100.0	166	4 AAF30864	Consensus human le
18	42	100.0	166	4 AAF30865	Consensus human le
19	42	100.0	166	4 AAF30866	Consensus human le
20	42	100.0	166	6 AAF50229	Interferon alpha-1
21	42	100.0	166	7 AAF60828	Sequence of interf
22	42	100.0	166	7 AAF60100	Sequence of hybrid
23	42	100.0	166	7 AAF60102	Sequence of hybrid
24	42	100.0	166	7 AAF60103	Sequence of interf
25	42	100.0	166	7 AAF60304	Sequence of interf
26	42	100.0	166	10 AAP90186	Hybrid alpha-inter
27	42	100.0	166	10 AAP90188	Hybrid alpha-inter
28	42	100.0	166	10 AAP90189	Hybrid alpha-inter
29	42	100.0	166	14 AAR42813	Lymphoblastoid int
30	42	100.0	166	16 AAR67761	Interferon-alpha-6
31	42	100.0	166	16 AAR67762	Interferon-alpha-7
32	42	100.0	166	18 AAW43380	A human interferon
33	42	100.0	166	20 AAY43491	Human interferon-a
34	42	100.0	166	20 AAY05806	Human interferon-a
35	42	100.0	166	20 AAY05807	Human interferon-a
36	42	100.0	166	20 AAY05808	Human interferon-a
37	42	100.0	166	20 AAY05809	Human interferon-a
38	42	100.0	166	20 AAY05810	Human interferon-a
39	42	100.0	166	20 AAY05811	Human interferon-a
40	42	100.0	166	20 AAY05812	Human interferon-a
41	42	100.0	166	21 AAB07339	Mature human IFNal
42	42	100.0	166	21 AAB07341	Mutant human IFNal
43	42	100.0	166	21 AAB07345	Mutant human IFNal
44	42	100.0	166	21 AAB07345	Mutant human IFNal
45	42	100.0	166	21 AAB07346	Mutant human IFNal

## ALIGNMENTS

RESULT 1  
AAR47561  
ID AAR47561 standard; peptide; 11 AA.  
XX  
AC AAR47561;  
XX  
DT 12-JUL-1994 (first entry)  
XX  
DE Interferon-receptor binding peptide #4.  
XX  
DE IFN; cell surface receptor; pharmaceutical carrier molecule;  
KW drug delivery; neoplastic tissue; infection;  
KW Type I human interferon receptor complex.  
XX  
OS Synthetic.  
XX  
PN W09401457-A.  
XX  
PD 20-JAN-1994.  
XX  
PF 06-JUL-1993; 93WO-CA00279.  
XX  
PR 07-JUL-1992; 92US-0909739.  
XX  
PR 20-NOV-1992; 92US-0980525.  
(FISH/) FISH E N.  
PI Fish EN;  
PI WPI; 1994-034987/04.  
DR  
PT New interferon receptor-binding peptide(s) - useful for  
PT delivering a pharmaceutically active drug to cells, e.g.  
PT neoplastic, infected or inflamed tissue cells

XX PS Claim 4; Page 35; Slipp; English.

XX CC The critical clusters of amino acids in the different IFN-alphas and  
CC IFN-beta that interact with the Type 1 IFN receptor complex were  
CC defined. These critical peptide domains were used to design  
CC synthetic peptides AAR47558-R47564 that are useful as carriers for  
CC pharmaceutical compositions.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 42; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.075;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTEKKYSP 8  
|||||||

DB 2 ltekkysp 9

RESULT 2

ID AAR47562 standard; peptide; 18 AA.

XX AC AAR47562;

XX DT 12-JUL-1994 (first entry)

XX DE Interferon-receptor binding peptide #5.

XX KW IFN; cell surface receptor; pharmaceutical carrier molecule;  
KW drug delivery; neoplastic tissue; infection;  
KW Type 1 human interferon receptor complex.

XX OS Synthetic.

XX PN WO9401457-A.

XX PD 20-JAN-1994.

XX PF 06-JUL-1993; 93WO-CA00279.

XX PR 07-JUL-1992; 92US-0909739.

XX PS 20-NOV-1992; 92US-0980525.

XX PA (FISH/) FISH E N.

XX PI Fish EN;

XX DR WPI; 1994-034987/04.

XX FT New interferon receptor-binding peptide(s) - useful for  
FT delivering a pharmaceutically active drug to cells, e.g.  
FT neoplastic, infected or inflamed tissue cells

XX PS Claim 5; Page 35; Slipp; English.

XX CC The critical clusters of amino acids in the different IFN-alphas and  
CC IFN-beta that interact with the Type 1 IFN receptor complex were  
CC defined. These critical peptide domains were used to design  
CC synthetic peptides AAR47558-R47564 that are useful as carriers for  
CC pharmaceutical compositions.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 42; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTEKKYSP 8  
|||||||

DB 9 ltekkysp 16

RESULT 3

ID AAY55987 standard; Protein; 90 AA.

XX AC AAY55987;

XX DT 15-MAR-2000 (first entry)

XX DE Partial human interferon-alpha5 protein.

XX KW Antiviral; anticancer; antiproliferative; human; interferon-alpha5;  
KW hepatic disease; hepatitis C; viral cirrhosis; hepatocellular carcinoma;  
KW liver; gene expression.

XX OS Homo sapiens.

XX PN WO9558143-A1.

XX PD 18-NOV-1999.

XX PF 13-MAY-1999; 99WO-ES00134.

XX PR 13-MAY-1998; 98ES-0001003.

XX PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX PI Prieto Valtuena J, Civeira Murillo MP, Larrea Leoz E;

XX DR WPI; 2000-038959/03.

XX PS N-PSDB; AA247031.

XX FT Treating liver diseases with interferon-alpha5 or nucleic acid encoding  
FT it, particularly chronic hepatitis C

XX PS Disclosure; Page 30; 36pp; Spanish.

XX CC This sequence corresponds to a fragment of the human interferon-alpha5  
CC protein (Genbank Accession No: X02956). The invention relates to a  
CC method of using interferon-alpha5 or its coding sequence to prepare  
CC compositions for treatment of hepatic diseases, e.g. (i) chronic  
CC hepatitis C; (ii) cirrhosis of viral origin and (iii) hepatocellular  
CC carcinoma. The method restores the level of interferon-alpha5, which  
CC is reduced in diseased liver cells, to normal levels.

XX SQ Sequence 90 AA;

Query Match 100.0%; Score 42; DB 21; Length 90;

Best Local Similarity 100.0%; Pred. No. 0.68;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTEKKYSP 8

|||||||

DB 74 ltekkysp 81

RESULT 4

ID AAP20109 standard; Protein; 133 AA.

XX AC AAP20109;

XX DT 10-AUG-1992 (first entry)

XX DE Sequence encoded by leukocyte Interferon Leif G cDNA.

XX KW Viral infection; therapy; malignancy.

XX OS Homo sapiens.

XX XX

```

PN GB2079291-A.
XX
PD 20-JAN-1982.
XX
XX 01-JUL-1981; 81GB-0120279.
XX
XX 21-APR-1981; 81US-0256204.
PR PR 01-JUL-1980; 80US-0164986.
PR PR 08-SEP-1980; 80US-0184909.
PR PR 10-NOV-1980; 80US-0205578.
XX
XX (HOFF J) HOFFMANN-LA ROCHE AG.
PA (GENE-) GENENTECH INC.
PA
XX Goeddel DYN, Pestka S;
XX
XX WPI; 1982-04460E/03.
DR DR N-PSDB; AAN20096.
XX
XX Mature human leukocyte interferon polypeptide(s) - prepd. from
PT microbes transformed with appropriate DNA sequences
XX
XX Example; Fig 4; 20pp; English.
XX
XX The inventors claim a polypeptide comprising the AA sequence of a
CC mature human Leif and a DNA sequence encoding it. Leif A-D, F, H-J
CC and encoding DNA are specifically claimed. They are natural allelic
CC variations. Leif is isolated from the leukocytes of humans with
CC chronic myelogenous leukaemia, induced to produce interferon with
CC Sendai or Newcastle disease virus; esp. the cell line KG-1.
XX
XX Sequence 133 AA;
SQ

Query Match 100.0%; Score 42; DB 3; Length 133;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LREKYSKP 8
DB 98 ltekkysp 105

RESULT 5
AAR11799
ID AAR11799 standard; Protein; 150 AA.
XX
XX AAR11799;
XX
XX 03-JUN-1991 (first entry)
XX
XX Interferon alpha 88 as CR2 ligand.
XX
XX Cellular receptor 2; CR2; binding site; BS; auto-immune disease;
KW Epstein-Barr Virus; EBV; B lymphocyte; ligand; Interferon alpha 88.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Binding-site 72..86
FT /note= "fragment pref. included"
FT Binding-site 75..82
FT /note= "fragment most pref. included"
XX
XX WO9103251-A.
PN
XX 21-MAR-1991.
XX
XX 04-SEP-1990; 90WO-US05027.
XX
XX 20-APR-1990; 90US-0512118.
PR PR 08-SEP-1989; 89US-0404679.
XX
XX

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PA (CALB-) CALIF INST BIOLOGIC.
XX
XX Lernhardt W;
XX
XX WPI; 1991-101864/14.
XX
XX DNA segment encoding CR-2 ligand and CR2 binding site - used to
PT treat auto-immune disease. B-cell lymphoma and inhibit
PT Epstein-Barr virus infection
XX
XX Disclosure; Fig 2; 129pp; English.
XX
XX The ligand pref. includes the fragment indicated in the features.
CC The ligand pref. contains only a single BS and has an amino acid
CC sequence <100 (pref. <20) residues in length.
CC The ligand may also comprise a plurality of fragment 75..82.
CC A therapeutic compsn. contg. the polypeptide is used to stimulate
CC or inhibit B lymphocyte proliferation in patients with B cell
CC lymphoma. B lymphocytes and myeloma's can be stimulated in
CC patients with immunodeficiencies and immunoglobulin secretion by
CC hybridoma cultures can be boosted.
CC The compsn. can be administered to inhibit infection in vitro or in
CC vivo by Epstein-Barr Virus.
CC See also AAQ11140-42 and AAR11355 for IFN alpha.
XX
XX Sequence 150 AA;
SQ

Query Match 100.0%; Score 42; DB 12; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LREKYSKP 8
DB 115 ltekkysp 122

RESULT 6
AAP50168
ID AAP50168 standard; Protein; 162 AA.
XX
XX AAP50168;
XX
XX 30-OCT-1991 (first entry)
XX
XX Sequence of hybrid alpha interferon (alpha-IFN).
XX
XX Antiviral agent; antitumour; interferon-alpha; virucide;
KW Immunostimulant.
XX
XX Homo sapiens.
OS
XX
XX EP146903-A.
PN
XX 03-JUL-1985.
PD
XX
XX 17-DEC-1984; 84EP-0115623.
XX
XX 21-DEC-1983; 83US-0564066.
PR PR 19-DEC-1983; 83US-0562639.
XX
XX (SCHE ) SCHERING CORP.
PA
XX
XX Leibowitz PJ, Ryan MJ;
PT WPI; 1985-160612/27.
DR DR N-PSDB; AAN50236.
XX
XX New hybrid alpha-interferon with enhanced antiviral activity -
PT prepd. by recombinant DNA procedures
XX
XX Claim 2; Page 22; 26pp; English.
XX

```

CC The hybrid alpha-IFN of the invention includes different portions of  
 CC two different naturally occurring alpha-IFN as joined discrete sub-  
 CC sequences. They are defined and arranged as a delta-4 alpha-2  
 CC (Bgl II-1) sub-segment preceding a (Bgl II) alpha-1 segment. It has  
 CC an antiviral activity of at least 100,000 units/mg by cytopathic  
 CC effect-inhibition assay. Dose is 100,000 - 1000,000 units/square  
 CC metre body surface daily topically. The N-terminal Met is optional.  
 CC The claimed DNA sequence coding for the hybrid alpha-IFN may differ  
 CC in accordance with the degeneracy of the genetic code.

XX SQ Sequence 162 AA;

Query Match 100.0%; Score 42; DB 6; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTKKYSP 8  
 |||||  
 Db 127 ltekkysp 134

RESULT 7

ID AAP30687 standard; Protein; 165 AA.

XX AC AAP30687;

XX DT 10-SEP-1992 (first entry)

XX DE Thr14, Met16 mutant human leukocyte interferon subtype F.

XX KW Mutation; human; IFN.

XX OS Synthetic.

XX FH Key Location/Qualifiers  
 XX FT Region 14  
 XX FT /note= "mutation, Ala -> Thr"  
 XX FT Region 16  
 XX FT /note= "mutation, Ile -> Met"

XX PN W08304053-A.

XX PD 24-NOV-1983.

XX PF 25-APR-1983; 83WO-US00605.

XX PR 15-APR-1983; 83US-0483451.

XX PR 06-MAY-1984; 82US-0373494.

XX PR 12-DEC-1983; 83US-0360495.

XX PR 21-SEP-1987; 87US-0099096.

XX PR 01-JAN-1990; 90EP-0124236.

XX FA (AMGE-) AMGEN INC.

XX FA (AMGE-) AMGEN.

XX FA (MOLE-) APPL MOLECULAR GENE.

XX PI Alton NK, Peters MA, Stabinsky Y, Snitman DL;

XX PD WPI; 1983-833208/48.

XX PT Construction of large structural genes - useful in prepn. of

XX PT human leukocyte interferon and analogues

XX PS Claim 46; Page 85; 94pp; English.

XX CC The sequence is that of a polypeptide which differs from human

XX CC leukocyte interferon subtype F by two amino acid substitutions.

XX CC It may be recombinantly produced in micro organisms transformed

XX CC with the manufactured gene encoding it. See also AAP30673-P30686.

XX SQ Sequence 165 AA;

Query Match 100.0%; Score 42; DB 4; Length 165;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTKKYSP 8  
 |||||  
 Db 131 ltekkysp 138

RESULT 8

ID AAW43382

XX AC AAW43382 standard; protein; 165 AA.

XX AC AAW43382;

XX DT 07-APR-1998 (first entry)

XX DE Human Interferon-alpha 2b mutant (K132T).

XX KW Gene delivery; Interferon-alpha 2b; IFN-alpha 2b; IFN-beta; IFN-gamma;

XX OS nucleic acid binding agent; targeted expression; mutant.

XX OS Homo sapiens.

XX PN W09733998-A1.

XX PD 18-SEP-1997.

XX PF 14-MAR-1997; 97WO-US03846.

XX PR 14-MAR-1996; 96US-0616023.

XX PR (IMMU-) IMMUNE RESPONSE CORP.

XX PI Carlo DJ, Chlou HC;

XX PD WPI; 1997-470878/43.

XX PT Delivering interferon gene to target mammalian cells in vivo or in  
 XX PT vitro - as a molecular complex with a conjugate of nucleic acid  
 XX PT binding agent and ligand for cell surface receptor, e.g. for  
 XX PT treating virus infection or tumours

XX PS Disclosure: Figure 11B; 52pp; English.

XX CC This sequence represents a human interferon-alpha 2b (IFN-alpha 2b)  
 XX CC mutant (K132T) which was recombinantly expressed in mice. A series  
 XX CC of IFN-alpha 2b mutants were prepared with various substitutions on  
 XX CC substitutions (AAW43382-90). The effect of these substitutions on  
 XX CC antiviral activity (on mouse cells) for human IFN-alpha 2b was  
 XX CC compared. This mutant had a relative activity of 0.1 compared with  
 XX CC the native IFN-alpha 2b. The invention relates to a complex which  
 XX CC targets expression of interferon in selected cells. The complex  
 XX CC comprises the gene encoding interferon releasably linked to a conjugate  
 XX CC of nucleic acid binding agent and a ligand which binds to a component on  
 XX CC the surface of the cell. The method is used for targeted expression of  
 XX CC recombinant IFN in selected cells, in vivo or in vitro, particularly for  
 XX CC treatment of hepatitis, several forms of cancer and leukaemia and  
 XX CC condyloma acuminatum, or for production of IFN for subsequent  
 XX CC administration as exogenous protein.

XX SQ Sequence 165 AA;

Query Match 100.0%; Score 42; DB 18; Length 165;

Best Local Similarity 100.0%; Pred. No. 1.3;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTKKYSP 8  
 |||||  
 Db 130 ltekkysp 137

```

RESULT 9
AAW43386
ID AAW43386 standard; protein; 165 AA.
AC AAW43386;
XX
XX
XX 07-APR-1998 (first entry)
DE
XX Human interferon-alpha 2b mutant (Q125R; K132T).
XX
XX Gene delivery; interferon-alpha 2b; IFN-alpha 2b; IFN-beta; IFN-gamma;
KW nucleic acid binding agent; targeted expression; mutant.
XX
XX Homo sapiens.
XX
XX W09733998-A1.
XX
XX 18-SEP-1997.
XX
XX 14-MAR-1997; 97MO-US03846.
XX
XX 14-MAR-1996; 96US-0616023.
XX
XX (IMMU-) IMMUNE RESPONSE CORP.
XX
XX Carlo DJ, Chiou HC;
XX
XX WPI; 1997-470878/43.
XX
XX Delivering interferon gene to target mammalian cells in vivo or in
PT vitro - as a molecular complex with a conjugate of nucleic acid
PT binding agent and ligand for cell surface receptor, e.g. for
PT treating virus infection or tumours
XX
XX Disclosure: Figure 11B; 52pp; English.
XX
XX This sequence represents a human interferon-alpha 2b (IFN-alpha 2b)
CC mutant (Q125R; K132T) which was recombinantly expressed in mice. A
CC series of IFN-alpha 2b mutants were prepared with various amino acid
CC substitutions (AAW43382-90). The effect of these substitutions on
CC antiviral activity (on mouse cells) for human IFN-alpha 2b was
CC compared. This mutant had a relative activity of 23 compared with
CC the native IFN-alpha 2b. The invention relates to a complex which
CC targets expression of interferon in selected cells. The complex
CC comprises the gene encoding interferon releasably linked to a conjugate
CC of nucleic acid binding agent and a ligand which binds to a component on
CC the surface of the cell. The method is used for targeted expression of
CC recombinant IFN in selected cells, in vivo or in vitro, particularly for
CC treatment of hepatitis, several forms of cancer and leukaemia and
CC condyloma acuminatum, or for production of IFN for subsequent
CC administration as exogenous protein.
XX
XX Sequence 165 AA;
SQ
Query Match 100.0%; Score 42; DB 18; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSKP 8
DB 130 ltekkysp 137

RESULT 10
AAW43387
ID AAW43387 standard; protein; 165 AA.
AC AAW43387;
XX
XX 07-APR-1998 (first entry)
DE
XX
XX Human interferon-alpha 2b mutant (Q125K; K132T).
XX
XX Gene delivery; interferon-alpha 2b; IFN-alpha 2b; IFN-beta; IFN-gamma;
KW nucleic acid binding agent; targeted expression; mutant.
XX
XX Homo sapiens.
XX
XX W09733998-A1.
XX
XX 18-SEP-1997.
XX
XX 14-MAR-1997; 97MO-US03846.
XX
XX 14-MAR-1996; 96US-0616023.
XX
XX (IMMU-) IMMUNE RESPONSE CORP.
XX
XX Carlo DJ, Chiou HC;
XX
XX WPI; 1997-470878/43.
XX
XX Delivering interferon gene to target mammalian cells in vivo or in
PT vitro - as a molecular complex with a conjugate of nucleic acid
PT binding agent and ligand for cell surface receptor, e.g. for
PT treating virus infection or tumours
XX
XX Disclosure: Figure 11B; 52pp; English.
XX
XX This sequence represents a human interferon-alpha 2b (IFN-alpha 2b)
CC mutant (Q125R; K132T) which was recombinantly expressed in mice. A
CC series of IFN-alpha 2b mutants were prepared with various amino acid
CC substitutions (AAW43382-90). The effect of these substitutions on
CC antiviral activity (on mouse cells) for human IFN-alpha 2b was
CC compared. This mutant had a relative activity of 23 compared with
CC the native IFN-alpha 2b. The invention relates to a complex which
CC targets expression of interferon in selected cells. The complex
CC comprises the gene encoding interferon releasably linked to a conjugate
CC of nucleic acid binding agent and a ligand which binds to a component on
CC the surface of the cell. The method is used for targeted expression of
CC recombinant IFN in selected cells, in vivo or in vitro, particularly for
CC treatment of hepatitis, several forms of cancer and leukaemia and
CC condyloma acuminatum, or for production of IFN for subsequent
CC administration as exogenous protein.
XX
XX Sequence 165 AA;
SQ
Query Match 100.0%; Score 42; DB 18; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSKP 8
DB 130 ltekkysp 137

```

```

XX Human interferon-alpha 2b mutant (R121K; Q125R; K132T).
XX
XX Gene delivery; interferon-alpha 2b; IFN-alpha 2b; IFN-beta; IFN-gamma;
KW nucleic acid binding agent; targeted expression; mutant.
XX
XX Homo sapiens.
XX
XX W09733998-A1.
XX
XX 18-SEP-1997.
XX
XX 14-MAR-1997; 97MO-US03846.
XX
XX 14-MAR-1996; 96US-0616023.
XX
XX (IMMU-) IMMUNE RESPONSE CORP.
XX
XX Carlo DJ, Chiou HC;
XX
XX WPI; 1997-470878/43.
XX
XX Delivering interferon gene to target mammalian cells in vivo or in
PT vitro - as a molecular complex with a conjugate of nucleic acid
PT binding agent and ligand for cell surface receptor, e.g. for
PT treating virus infection or tumours
XX
XX Disclosure: Figure 11B; 52pp; English.
XX
XX This sequence represents a human interferon-alpha 2b (IFN-alpha 2b)
CC mutant (R121K; Q125R; K132T) which was recombinantly expressed in mice.
CC A series of IFN-alpha 2b mutants were prepared with various amino acid
CC substitutions (AAW43382-90). The effect of these substitutions on
CC antiviral activity (on mouse cells) for human IFN-alpha 2b was
CC compared. This mutant had a relative activity of 170 compared with
CC the native IFN-alpha 2b. The invention relates to a complex which
CC targets expression of interferon in selected cells. The complex
CC comprises the gene encoding interferon releasably linked to a conjugate
CC of nucleic acid binding agent and a ligand which binds to a component on
CC the surface of the cell. The method is used for targeted expression of
CC recombinant IFN in selected cells, in vivo or in vitro, particularly for
CC treatment of hepatitis, several forms of cancer and leukaemia and
CC condyloma acuminatum, or for production of IFN for subsequent
CC administration as exogenous protein.
XX
XX Sequence 165 AA;
SQ
Query Match 100.0%; Score 42; DB 18; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSKP 8
DB 130 ltekkysp 137

RESULT 11
AAW43390
ID AAW43390 standard; protein; 165 AA.
XX
XX AAW43390;
XX
XX 07-APR-1998 (first entry)
XX
XX Human interferon-alpha 2b mutant (Q125K; K132T).
XX
XX Gene delivery; interferon-alpha 2b; IFN-alpha 2b; IFN-beta; IFN-gamma;
KW nucleic acid binding agent; targeted expression; mutant.
XX
XX Homo sapiens.
XX
XX W09733998-A1.

```

XX PD 18-SEP-1997.  
XX PF 14-MAR-1997; 97WO-US03846.  
XX PR 14-MAR-1996; 96US-0616023.  
XX PA (IMMU-) IMMUNE RESPONSE CORP.  
XX PI Carlo DJ, Chlou HC;  
XX DR WPI; 1997-470878/43.  
XX PT Delivering interferon gene to target mammalian cells in vivo or in  
XX PT vitro - as a molecular complex with a conjugate of nucleic acid  
XX PT binding agent and ligand for cell surface receptor, e.g. for  
XX PT treating virus infection or tumours  
XX PS Disclosure; Figure 11B; 52pp; English.  
XX CC This sequence represents a human interferon-alpha 2b (IFN-alpha 2b)  
XX CC mutant (Q125K; K132T) which was recombinantly expressed in mice. A  
XX CC series of IFN-alpha 2b mutants were prepared with various amino acid  
XX CC substitutions (AAM43382-90). The effect of these substitutions on  
XX CC antiviral activity (on mouse cells) for human IFN-alpha 2b was  
XX CC compared. This mutant had a relative activity of 45 compared with  
XX CC the native IFN-alpha 2b. The invention relates to a complex which  
XX CC targets expression of interferon in selected cells. The complex  
XX CC comprises the gene encoding interferon releasably linked to a conjugate  
XX CC of nucleic acid binding agent and a ligand which binds to a component on  
XX CC the surface of the cell. The method is used for targeted expression of  
XX CC recombinant IFN in selected cells, in vivo or in vitro, particularly for  
XX CC treatment of hepatitis, several forms of cancer and leukaemia and  
XX CC condyloma acuminatum, or for production of IFN for subsequent  
XX CC administration as exogenous protein.  
XX SQ Sequence 165 AA;

Query Match 100.0%; Score 42; DB 18; Length 165;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LTERKYPSP 8  
Db 130 ltekkypsp 137  
|||||

RESULT 12  
AAV43492  
ID AAY43492 standard; Protein; 165 AA.  
XX AC AAY43492;  
XX DT 26-JAN-2000 (first entry)  
XX DE A human interferon-alpha (IFN-alpha) protein.  
XX KW Interferon-alpha-2b; IFN-alpha; avb3 antagonist; avb3 receptor ligand;  
XX KW metastasis-associated receptor ligand; angiogenesis; cell proliferation;  
XX KW anti-angiogenic protein; avb3-integrin; cancer; arthritis;  
XX KW macular degeneration; diabetic retinopathy; hemangioma; psoriasis;  
XX KW osteoporosis; thrombosis; angina; atherosclerosis; antiviral;  
XX KW antibacterial; antifungal.  
XX OS Homo sapiens.  
XX PN WO9951638-A1.  
XX PD 14-OCT-1999.  
XX PF 07-APR-1999; 99WO-US04295.  
XX PI

PR 08-APR-1998; 98US-0081074.  
XX PA (SEAR ) SEARLE & CO G D.  
XX PI Tjoeng FS, Fok KF;  
XX DR WPI; 1999-620196/53.  
XX PT New conjugates of integrin antagonist and ligand for  
XX PT metastasis-associated receptor, for treating angiogenesis-related  
XX PT diseases, e.g. cancer  
XX PS Claim 12; Page 102; 108pp; English.  
XX CC The present sequence represents an interferon-alpha (IFN-alpha) protein,  
XX CC and can be conjugated to the avb3 antagonists of the invention. The  
XX CC specification describes pharmaceutical compounds and their salts which  
XX CC are dual avb3 receptor/metastasis-associated receptor ligands. These  
XX CC compounds inhibit angiogenesis and thus proliferation of (cancer) cells.  
XX CC One component binds to the avb3 receptor and the other to a  
XX CC metastasis-associated receptor. The avb3 antagonists may also be  
XX CC conjugated to anti-angiogenic proteins, such as IFN-alpha and its  
XX CC derivatives. The compounds are used to treat angiogenesis-related  
XX CC disorders (mediated by the avb3-integrin), specifically cancer (of lung,  
XX CC breast, ovary, prostate, stomach, colon, kidney or bladder, also  
XX CC melanoma, hepatoma, sarcoma and lymphoma), arthritis and macular  
XX CC degeneration, and also diabetic retinopathy, hemangioma, psoriasis,  
XX CC osteoporosis, thrombosis, angina, atherosclerosis etc. The compounds may  
XX CC also be useful as antiviral, antibacterial and antifungal agents.  
XX SQ Sequence 165 AA;

Query Match 100.0%; Score 42; DB 20; Length 165;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LTERKYPSP 8  
Db 130 ltekkypsp 137  
|||||

RESULT 13  
AAV82887  
ID AAY82887 standard; Protein; 165 AA.  
XX AC AAY82887;  
XX DT 25-JUL-2000 (first entry)  
XX DE N-terminal modified interferon alpha A/D hybrid.  
XX KW Biconjugate; a\_vb3 integrin; interferon alpha; angiogenesis;  
XX KW cancer; tumour; osteoporosis; Paget's disease; Kaposi's sarcoma;  
XX KW periodontal disease; metastasis; neoplasia; retinopathy; arthritis;  
XX KW psoriasis; leukaemia; malignant melanoma; atherosclerosis;  
XX KW smooth muscle cell migration; inhibition; treatment; antagonist;  
XX KW angina; thrombosis; restenosis; antiviral; antifungal;  
XX KW antibacterial.  
XX OS Homo sapiens.  
XX PN WO200009143-A1.  
XX PD 24-FEB-2000.  
XX PF 07-APR-1999; 99WO-US04296.  
XX PR 13-AUG-1998; 98US-0096442.  
XX PA (SEAR ) SEARLE & CO G D.  
XX PI Fok KF, Tjoeng FS;



10-FEB-2000.

06-JUL-1999; 99WO-US15284.

28-JUL-1998; 98US-0094407.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Zoon KC, Hu R, Bekisz JB, Hayes MP;

WPI; 2000-183128/16.

N-PSDB; AA250311.

New hybrid interferon-alpha polypeptides with interferon-alpha biological activity, useful to treat viral diseases

Claim 8; Fig 5; 72pp; English.

The present sequence is hybrid interferon fusion protein HY-3, comprising IFN-alpha 2c (amino acid residues 96-166) and IFN-alpha21a (amino acid residues 1-95). This is used as an antiviral and antiproliferative agent. Hybrid IFN-alpha (interferon-alpha) proteins are used in the treatment of viral diseases e.g. influenza, hepatitis B, or to regulate cell growth, especially tumour cell growth e.g. in tumour treatment and cancers like osteogenic sarcoma, multiple myeloma etc. They are transformed into host cells using vectors. Pharmaceutically acceptable carriers can be included with hybrid IFN-alpha for therapeutic administration.

Sequence 165 AA;

Query Match 100.0%; Score 42; DB 21; Length 165;  
Best Local Similarity 100.0%; Pred. No. 1.3; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0;

QY 1 LTKKYSP 8  
| | | | | | | |  
Db 130 ltekkysp 137

RESULT 15  
AAAY44976  
ID AAAY44976 standard; Protein; 165 AA.  
AC AAAY44976;  
XX  
XX  
DT 23-MAY-2000 (first entry)  
XX  
XX  
DE Human hybrid interferon alpha, HY-3.  
XX  
XX  
KW Human; Interferon alpha; HuIFNalpha; hybrid; HY-3; IFN-alpha21a; tumour;  
KW IFN-alpha2c; cytostatic; antiviral; antiproliferative; immunomodulator;  
KW treatment; viral disease; encephalomyocarditis; influenza; rabies;  
KW respiratory tract infection; viral zoonoses; arbovirus infection;  
KW Herpes simplex; Varicella zoster; keratitis; Hodgkin's disease; cancer;  
KW acute haemorrhagic conjunctivitis; hepatitis B; hepatitis C; lymphoma;  
KW osteogenic sarcoma; multiple myeloma; leukaemia; carcinoma; melanoma;  
KW papilloma.  
XX  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FH Region 1..95  
FT /note= "Derived from IFN-alpha2c"  
FT Domain 76..166  
FT /note= "Domain affecting antiproliferative activity"  
FT Region 96..166  
FT /note= "Derived from IFN-alpha21a"  
XX  
XX  
PN WO200006596-A2.

10-FEB-2000.

06-JUL-1999; 99WO-US15284.

28-JUL-1998; 98US-0094407.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Zoon KC, Hu R, Bekisz JB, Hayes MP;

WPI; 2000-183128/16.

N-PSDB; AA250311.

New hybrid interferon-alpha polypeptides with interferon-alpha biological activity, useful to treat viral diseases

Claim 8; Fig 5; 72pp; English.

The present sequence is hybrid interferon fusion protein HY-3, comprising IFN-alpha 2c (amino acid residues 96-166) and IFN-alpha21a (amino acid residues 1-95). This is used as an antiviral and antiproliferative agent. Hybrid IFN-alpha (interferon-alpha) proteins are used in the treatment of viral diseases e.g. influenza, hepatitis B, or to regulate cell growth, especially tumour cell growth e.g. in tumour treatment and cancers like osteogenic sarcoma, multiple myeloma etc. They are transformed into host cells using vectors. Pharmaceutically acceptable carriers can be included with hybrid IFN-alpha for therapeutic administration.

Sequence 165 AA;

Query Match 100.0%; Score 42; DB 21; Length 165;  
Best Local Similarity 100.0%; Pred. No. 1.3; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0;

QY 1 LTKKYSP 8  
| | | | | | | |  
Db 130 ltekkysp 137

RESULT 14  
AAAY44828  
ID AAAY44828 standard; Protein; 165 AA.  
AC AAAY44828;  
XX  
XX  
DT 18-MAY-2000 (first entry)  
XX  
XX  
DE Hybrid interferon fusion protein HY-3.  
XX  
XX  
KW Hybrid interferon-alpha protein; HY-3; IFN-alpha; antiviral;  
KW antiproliferative; influenza; hepatitis B; cell growth regulation;  
KW tumour; cancer; osteogenic sarcoma; multiple myeloma.  
XX  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
XX  
PN WO200006735-A1.

PD 10-FEB-2000.  
 XX  
 PF 29-JUN-1999; 99WO-US14749.  
 XX  
 PR 28-JUL-1998; 98US-0094407.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Zoon KC, Hu R, Bekisz JB, Hayes MP;  
 XX  
 DR WPI; 2000-195259/17.  
 DR N-PSDB; AA250512.  
 XX  
 PT Novel human hybrid interferons and their mutants, useful for treating  
 PT viral infections such as rabies and hepatitis B and C, and cancers such  
 PT as melanoma, multiple myeloma, and papilloma  
 XX  
 PS Claim 10; Page 49-50; 66pp; English.  
 CC  
 CC The present amino acid sequence is the human hybrid interferon-alpha  
 CC (HuIFNalpha) polypeptide HY-3, comprising a fusion of IFN-alpha21a and  
 CC IFN-alpha2c. This hybrid IFN has antiviral, antiproliferative,  
 CC cytostatic and immunomodulator activity. HY-3 exhibited a higher  
 CC antiproliferative activity than the parental interferons, IFN-alpha2c  
 CC and IFN-alpha21a and other IFN-alpha hybrids.  
 CC Hybrid IFNs are used for treatment of viral diseases, such as  
 CC encephalomyocarditis, influenza, respiratory tract infections, rabies,  
 CC viral zoonoses, arbovirus, Herpes simplex and Varicella zoster  
 CC infections, keratitis, acute haemorrhagic conjunctivitis and hepatitis B  
 CC and C. It is also used for modulation of immune system, regulation of  
 CC tumour growth and cancers such as osteogenic sarcoma, multiple myeloma,  
 CC Hodgkin's disease, nodular, poorly differentiated lymphoma, acute  
 CC lymphocytic leukaemia, acute myeloid leukaemia, breast carcinoma,  
 CC melanoma, papilloma and nasopharyngeal carcinoma in humans.  
 XX  
 SQ Sequence 165 AA;

Query Match 100.0%; Score 42; DB 21; Length 165;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 LTKKYP 8  
 Db 130 ltekkyp 137  
 |||||

Search completed: December 13, 2001, 10:46:23  
 Job time: 101 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 13, 2001, 10:44:40 ; Search time 181.51 Seconds

(without alignments)  
12.238 Million cell updates/sec

Title: US-09-424-080A-1

Perfect score: 42

Sequence: 1 LTERKYSK 8

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2\_6/ptodata/2/paa/PCTUS\_COMB.pep.\*
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- 3: /cgn2\_6/ptodata/2/paa/US07\_COMB.pep.\*
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- 5: /cgn2\_6/ptodata/2/paa/US081\_COMB.pep.\*
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- 10: /cgn2\_6/ptodata/2/paa/US086\_COMB.pep.\*
- 11: /cgn2\_6/ptodata/2/paa/US087\_COMB.pep.\*
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- 13: /cgn2\_6/ptodata/2/paa/US089\_COMB.pep.\*
- 14: /cgn2\_6/ptodata/2/paa/US090\_COMB.pep.\*
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- 19: /cgn2\_6/ptodata/2/paa/US095\_COMB.pep.\*
- 20: /cgn2\_6/ptodata/2/paa/US096\_COMB.pep.\*
- 21: /cgn2\_6/ptodata/2/paa/US097\_COMB.pep.\*
- 22: /cgn2\_6/ptodata/2/paa/US098\_COMB.pep.\*
- 23: /cgn2\_6/ptodata/2/paa/US099\_COMB.pep.\*
- 24: /cgn2\_6/ptodata/2/paa/US60\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	8	18	US-09-424-080-1
2	42	100.0	11	3	US-07-980-525-4
3	42	100.0	11	13	US-08-920-579-4
4	42	100.0	18	3	US-07-980-525-5
5	42	100.0	18	13	US-08-920-579-5
6	42	100.0	30	11	US-08-769-062-79
7	42	100.0	46	24	US-60-182-467-1317
8	42	100.0	60	24	US-60-163-123-1406
9	42	100.0	70	24	US-60-177-571-2851

Sequence 2858, Ap  
Sequence 11, Appl  
Sequence 2852, Ap  
Sequence 2853, Ap  
Sequence 2854, Ap  
Sequence 2855, Ap  
Sequence 2856, Ap  
Sequence 2857, Ap  
Sequence 2859, Ap  
Sequence 2860, Ap  
Sequence 2861, Ap  
Sequence 2862, Ap  
Sequence 1760, Ap  
Sequence 5609, Ap  
Sequence 14, Appl  
Sequence 23, Appl  
Sequence 1012, Ap  
Sequence 1197, Ap  
Sequence 10, Appl  
Sequence 12, Appl  
Sequence 10, Appl  
Sequence 11, Appl  
Sequence 12, Appl  
Sequence 15, Appl  
Sequence 15, Appl  
Sequence 5608, Ap  
Sequence 5607, Ap  
Sequence 5610, Ap  
Sequence 5611, Ap  
Sequence 5613, Ap  
Sequence 13, Appl  
Sequence 14, Appl  
Sequence 13, Appl  
Sequence 14, Appl  
Sequence 28, Appl

US-60-177-571-2858  
US-09-275-278-11  
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US-60-177-571-2853  
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US-60-177-571-2861  
US-60-177-571-2862  
US-60-163-123-1760  
US-60-196-718-5609  
US-06-256-204-14  
US-06-256-204-23  
US-60-163-123-1012  
US-60-163-123-1197  
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US-07-980-525-11  
US-07-980-525-12  
US-08-920-579-10  
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US-08-920-579-12  
US-07-980-525-15  
US-08-920-579-15  
US-60-196-718-5608  
US-60-196-718-5607  
US-60-196-718-5610  
US-60-196-718-5611  
US-60-196-718-5613  
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US-07-980-525-14  
US-08-920-579-13  
US-08-920-579-14  
US-09-283-390-28

## ALIGNMENTS

RESULT 1  
US-09-424-080-1  
; Sequence 1, Application US/09424080  
; GENERAL INFORMATION:  
; APPLICANT: ZAVIAJOV, Vladimir et al.  
; TITLE OF INVENTION: COMPOSITION FOR ENHANCING IMMUNOSUPPRESSANTS PHARMACEUTICAL ACT  
; FILE REFERENCE: 0933-0149P  
; CURRENT APPLICATION NUMBER: US/09/424.080  
; CURRENT FILING DATE: 2000-02-14  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Immunosuppressants cycloporins, FK506, or rapamycin sequences  
; OTHER INFORMATION: derived from various organisms using sequence alignment.  
US-09-424-080-1

Query Match 100.0%; Score 42; DB 18; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.9e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LTERKYSK 8  
Db 1 LTERKYSK 8  
RESULT 2  
US-07-980-525-4

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; Sequence 4, Application US/07980525
; GENERAL INFORMATION:
; APPLICANT: FISH, Eleanor N.
; TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/980.525
; FILING DATE: 19921120
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/909.738
; FILING DATE: 07-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Murray, Robert B.
; REGISTRATION NUMBER: 22,980
; REFERENCE/DOCKET NUMBER: 638-2005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-07-980-525-4

Query Match 100.0%; Score 42; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

QY 1 LEEKKYP 8
Db 2 LEEKKYP 9

RESULT 3
US-08-920-579-4
; Sequence 4, Application US/08920579
; GENERAL INFORMATION:
; APPLICANT: Fish, Eleanor N.
; TITLE OF INVENTION: Interferon Receptor Binding Peptide
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/920.579
; FILING DATE: 29-AUG-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Rudolph, John R.
; REGISTRATION NUMBER: 38,003
; REFERENCE/DOCKET NUMBER: 7841-92
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-920-579-4

Query Match 100.0%; Score 42; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

QY 1 LEEKKYP 8
Db 2 LEEKKYP 9

RESULT 4
US-07-980-525-5
; Sequence 5, Application US/07980525
; GENERAL INFORMATION:
; APPLICANT: FISH, Eleanor N.
; TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/980.525
; FILING DATE: 19921120
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/909.738
; FILING DATE: 07-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Murray, Robert B.
; REGISTRATION NUMBER: 22,980
; REFERENCE/DOCKET NUMBER: 638-2005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-07-980-525-5

Query Match 100.0%; Score 42; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.2; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

QY 1 LEEKKYP 8
Db 2 LEEKKYP 9

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Db 9 LTEKKYSP 16

RESULT 5  
US-08-920-579-5  
; Sequence 5, Application US/08920579  
; GENERAL INFORMATION:  
; APPLICANT: Fish, Eleanor N.  
; TITLE OF INVENTION: Interferon Receptor Binding Peptide  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BEREKSIK & PARR  
; STREET: 40 King Street West  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5H 3Y2  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/920,579  
; FILING DATE: 29-AUG-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rudolph, John R.  
; REGISTRATION NUMBER: 38,003  
; REFERENCE/DOCKET NUMBER: 7841-92  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 364-7311  
; TELEFAX: (416) 361-1398  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-920-579-5

Query Match 100.0%; Score 42; DB 13; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTEKKYSP 8  
|||||||  
Db 9 LTEKKYSP 16

RESULT 6  
US-08-769-062-79  
; Sequence 79, Application US/08769062  
; GENERAL INFORMATION:  
; APPLICANT: Patten, Phillip  
; TITLE OF INVENTION: Methods and compositions for  
; TITLE OF INVENTION: Polypeptide engineering  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Affymax Research Institute  
; STREET: 4001 Miranda Avenue  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94024  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/769,062  
; FILING DATE: 18-DEC-1996  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/198,431  
; FILING DATE: 17-FEB-1994  
; APPLICATION NUMBER: 08/425,684  
; FILING DATE: 18-APR-1995  
; APPLICATION NUMBER: 08/537,874  
; FILING DATE: 30-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stevens, Lauren L.  
; REGISTRATION NUMBER: 36,691  
; REFERENCE/DOCKET NUMBER: 2026  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-812-8803  
; TELEFAX: 415-424-0832  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 79:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-769-062-79

Query Match 100.0%; Score 42; DB 11; Length 30;  
Best Local Similarity 100.0%; Pred. No. 0.36;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTEKKYSP 8  
|||||||  
Db 11 LTEKKYSP 18

RESULT 7  
US-60-182-467-1317  
; Sequence 1317, Application US/60182467  
; GENERAL INFORMATION:  
; APPLICANT: Bonazzi, Vivien  
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND  
; FILE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL000248  
; CURRENT APPLICATION NUMBER: US/60/182,467  
; CURRENT FILING DATE: 2000-02-15  
; NUMBER OF SEQ ID NOS: 2194  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1317  
; LENGTH: 46  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-60-182-467-1317

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Best Local Similarity 100.0%; Pred. No. 0.6;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTEKKYSP 8  
|||||||  
Db 13 LTEKKYSP 20

RESULT 8  
US-60-163-123-1406  
; Sequence 1406, Application US/60163123  
; GENERAL INFORMATION:  
; APPLICANT: Bonazzi, Vivien  
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND

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; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000137
; CURRENT APPLICATION NUMBER: US/60/163,123
; CURRENT FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 1986
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1406
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Human
US-60-163-123-1406

Query Match          100.0%; Score 42; DB 24; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSKP 8
Db 25 LTERKYSKP 32

RESULT 9
US-60-177-571-2851
; Sequence 2851, Application US/60177571
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
; FILE REFERENCE: CL000201
; CURRENT APPLICATION NUMBER: US/60/177,571
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 5082
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2851
; LENGTH: 70
; TYPE: PRT
; ORGANISM: HUMAN
US-60-177-571-2851

Query Match          100.0%; Score 42; DB 24; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSKP 8
Db 39 LTERKYSKP 46

RESULT 10
US-60-177-571-2858
; Sequence 2858, Application US/60177571
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
; FILE REFERENCE: CL000201
; CURRENT APPLICATION NUMBER: US/60/177,571
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 5082
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2858
; LENGTH: 71
; TYPE: PRT
; ORGANISM: HUMAN
US-60-177-571-2858

Query Match          100.0%; Score 42; DB 24; Length 71;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-60-177-571-2851
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSKP 8
Db 38 LTERKYSKP 45

RESULT 11
US-09-275-278-11
; Sequence 11, Application US/09275278
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Yeung, George
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: A NOVEL INTERFERON AND USES THEREOF
; FILE REFERENCE: 20411-772 (28110/16060)
; CURRENT APPLICATION NUMBER: US/09/275,278
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 09/137,348
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: US 09/034,878
; PRIOR FILING DATE: 1998-03-04
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-275-278-11

Query Match          100.0%; Score 42; DB 16; Length 72;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSKP 8
Db 65 LTERKYSKP 72

RESULT 12
US-60-177-571-2852
; Sequence 2852, Application US/60177571
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
; FILE REFERENCE: CL000201
; CURRENT APPLICATION NUMBER: US/60/177,571
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 5082
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2852
; LENGTH: 73
; TYPE: PRT
; ORGANISM: HUMAN
US-60-177-571-2852

Query Match          100.0%; Score 42; DB 24; Length 73;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSKP 8
Db 38 LTERKYSKP 45

RESULT 13
US-60-177-571-2853
; Sequence 2853, Application US/60177571
; GENERAL INFORMATION:
```

; APPLICANT: Bonazzi, Vivien  
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: CL000201  
; CURRENT APPLICATION NUMBER: US/60/177,571  
; CURRENT FILING DATE: 2000-01-27  
; NUMBER OF SEQ ID NOS: 5082  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2853  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-60-177-571-2853

Query Match 100.0%; Score 42; DB 24; Length 73;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKKYSP 8  
| | | | | | | |  
Db 38 LTERKKYSP 45

RESULT 14  
US-60-177-571-2854  
; Sequence 2854, Application US/60177571  
; GENERAL INFORMATION:  
; APPLICANT: Bonazzi, Vivien  
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CL000201  
; CURRENT APPLICATION NUMBER: US/60/177,571  
; CURRENT FILING DATE: 2000-01-27  
; NUMBER OF SEQ ID NOS: 5082  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2854  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-60-177-571-2854

Query Match 100.0%; Score 42; DB 24; Length 73;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKKYSP 8  
| | | | | | | |  
Db 38 LTERKKYSP 45

RESULT 15  
US-60-177-571-2855  
; Sequence 2855, Application US/60177571  
; GENERAL INFORMATION:  
; APPLICANT: Bonazzi, Vivien  
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CL000201  
; CURRENT APPLICATION NUMBER: US/60/177,571  
; CURRENT FILING DATE: 2000-01-27  
; NUMBER OF SEQ ID NOS: 5082  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2855  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-60-177-571-2855

Query Match 100.0%; Score 42; DB 24; Length 73;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKKYSP 8  
| | | | | | | |  
Db 38 LTERKKYSP 45

Search completed: December 13, 2001, 10:49:31  
Job time: 291 sec

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## OM protein - protein search, using sw model

Run on: December 13, 2001, 10:44:40 ; Search time 9.21 Seconds  
(without alignments)  
10.008 Million cell updates/sec

Title: US-09-424-080A-1

Perfect score: 42

Sequence: 1 LEEKYSP 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 61579 seqs, 11521160 residues

Total number of hits satisfying chosen parameters: 61579

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_AA\_New.\*

- 1: /cgn2.6/ptodata/1/paa/pct\_NEW\_COMB.pep.\*
- 2: /cgn2.6/ptodata/1/paa/US06\_NEW\_COMB.pep.\*
- 3: /cgn2.6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*
- 4: /cgn2.6/ptodata/1/paa/US08\_NEW\_COMB.pep.\*
- 5: /cgn2.6/ptodata/1/paa/US09\_NEW\_COMB.pep.\*
- 6: /cgn2.6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	8	5	US-09-424-080A-1
2	42	100.0	166	5	US-09-977-034-2
3	42	100.0	166	5	US-09-977-034-8
4	42	100.0	166	5	US-09-977-034-10
5	42	100.0	166	5	US-09-977-034-11
6	42	100.0	166	5	US-09-977-034-12
7	42	100.0	166	5	US-09-977-034-18
8	42	100.0	166	5	US-09-977-034-19
9	36	85.7	165	5	US-09-633-516B-13
10	36	85.7	165	5	US-09-633-516B-14
11	36	85.7	165	5	US-09-977-034-9
12	36	85.7	166	5	US-09-977-034-13
13	36	85.7	170	5	US-09-977-034-16
14	36	85.7	831	6	US-60-329-756-2
15	35	83.3	166	5	US-09-977-034-14
16	33	78.6	166	5	US-09-977-034-15
17	31	73.8	166	5	US-09-977-034-22
18	31	73.8	166	5	US-09-977-034-25
19	31	73.8	166	5	US-09-977-034-26
20	31	73.8	166	5	US-09-977-034-28
21	31	73.8	167	5	US-09-977-034-23
22	31	73.8	167	5	US-09-977-034-27
23	31	73.8	167	5	US-09-977-034-29
24	31	73.8	198	5	US-09-823-307-2
25	31	73.8	198	5	US-09-972-524-2
26	31	73.8	198	5	US-09-823-307A-2
27	31	73.8	427	5	US-09-897-516-7860

## ALIGNMENTS

## RESULT 1

US-09-424-080A-1

; Sequence 1, Application US/09424080A

; GENERAL INFORMATION:

; APPLICANT: ZAVIALOV, Vladimir et al.

; TITLE OF INVENTION: COMPOSITION FOR ENHANCING IMMUNOSUPPRESSANTS PHARMACEUTICAL ACT

; FILE REFERENCE: 0933-0149P

; CURRENT APPLICATION NUMBER: US/09/424,080A

; CURRENT FILING DATE: 2000-02-14

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: A peptide corresponding to the high-affinity binding/anti-

; OTHER INFORMATION: Lymphoproliferative

; OTHER INFORMATION: site of human IFN-alpha

US-09-424-080A-1

Query Match 100.0%; Score 42; DB 5; Length 8;  
Best Local Similarity 100.0%; Pred No. 5.4e+04;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEEKYSP 8

Db 1 LEEKYSP 8

## RESULT 2

US-09-977-034-2

; Sequence 2, Application US/09977034

; GENERAL INFORMATION:

; APPLICANT: Lo, Kin-Ming

; APPLICANT: Sun, Yaping

; APPLICANT: Gillies, Stephen D.

; TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as

; FILE REFERENCE: LEX-009

; CURRENT APPLICATION NUMBER: US/09/977,034

; CURRENT FILING DATE: 2001-10-11

; PRIOR APPLICATION NUMBER: US/09/575,503

; PRIOR FILING DATE: 2000-05-19

; PRIOR APPLICATION NUMBER: US 60/134,895

; PRIOR FILING DATE: 1999-05-19

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2



LENGTH: 166  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-977-034-2

Query Match 100.0%; Score 42; DB 5; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.067;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKKYSP 8  
Db 131 LTERKKYSP 138

RESULT 3  
US-09-977-034-8  
; Sequence 8, Application US/09977034  
; GENERAL INFORMATION:  
; APPLICANT: Lo, Kin-Ming  
; APPLICANT: Sun, Yaping  
; APPLICANT: Gillies, Stephen D.  
; TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as  
; FILE REFERENCE: LEX-009  
; CURRENT APPLICATION NUMBER: US/09/977,034  
; PRIOR FILING DATE: 2001-10-11  
; PRIOR APPLICATION NUMBER: US/09/575,503  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: US 60/134,895  
; PRIOR FILING DATE: 1999-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 166  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Human IFN alpha-1 protein  
US-09-977-034-8

Query Match 100.0%; Score 42; DB 5; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.067;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKKYSP 8  
Db 131 LTERKKYSP 138

RESULT 4  
US-09-977-034-10  
; Sequence 10, Application US/09977034  
; GENERAL INFORMATION:  
; APPLICANT: Lo, Kin-Ming  
; APPLICANT: Sun, Yaping  
; APPLICANT: Gillies, Stephen D.  
; TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as  
; FILE REFERENCE: LEX-009  
; CURRENT APPLICATION NUMBER: US/09/977,034  
; PRIOR FILING DATE: 2001-10-11  
; PRIOR APPLICATION NUMBER: US/09/575,503  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: US 60/134,895  
; PRIOR FILING DATE: 1999-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 166  
; TYPE: PRT  
; ORGANISM: Homo sapiens

FEATURE:  
OTHER INFORMATION: Human IFN alpha-4 protein  
US-09-977-034-10

Query Match 100.0%; Score 42; DB 5; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.067;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKKYSP 8  
Db 131 LTERKKYSP 138

RESULT 5  
US-09-977-034-11  
; Sequence 11, Application US/09977034  
; GENERAL INFORMATION:  
; APPLICANT: Lo, Kin-Ming  
; APPLICANT: Sun, Yaping  
; APPLICANT: Gillies, Stephen D.  
; TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as  
; FILE REFERENCE: LEX-009  
; CURRENT APPLICATION NUMBER: US/09/977,034  
; PRIOR FILING DATE: 2001-10-11  
; PRIOR APPLICATION NUMBER: US/09/575,503  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: US 60/134,895  
; PRIOR FILING DATE: 1999-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 166  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Human IFN alpha-5 protein  
US-09-977-034-11

Query Match 100.0%; Score 42; DB 5; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.067;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKKYSP 8  
Db 131 LTERKKYSP 138

RESULT 6  
US-09-977-034-12  
; Sequence 12, Application US/09977034  
; GENERAL INFORMATION:  
; APPLICANT: Lo, Kin-Ming  
; APPLICANT: Sun, Yaping  
; APPLICANT: Gillies, Stephen D.  
; TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as  
; FILE REFERENCE: LEX-009  
; CURRENT APPLICATION NUMBER: US/09/977,034  
; PRIOR FILING DATE: 2001-10-11  
; PRIOR APPLICATION NUMBER: US/09/575,503  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: US 60/134,895  
; PRIOR FILING DATE: 1999-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 166  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:

OTHER INFORMATION: Human IFN alpha-6 protein  
US-09-977-034-12

Query Match 100.0%; Score 42; DB 5; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.067;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSK 8  
| | | | | | | |  
Db 131 LTERKYSK 138

## RESULT 7

US-09-977-034-18  
; Sequence 18, Application US/09977034  
; GENERAL INFORMATION:  
; APPLICANT: LO, Kin-Ming  
; APPLICANT: Sun, Yaping  
; APPLICANT: Gillies, Stephen D.  
; TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as  
; TITLE OF INVENTION: FC Fusion Proteins  
; FILE REFERENCE: LEX-009  
; CURRENT APPLICATION NUMBER: US/09/977,034  
; PRIOR FILING DATE: 2001-10-11  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR FILING DATE: 1999-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 166  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Human IFN alpha-17 protein  
US-09-977-034-18

Query Match 100.0%; Score 42; DB 5; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.067;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSK 8  
| | | | | | | |  
Db 131 LTERKYSK 138

## RESULT 8

US-09-977-034-19  
; Sequence 19, Application US/09977034  
; GENERAL INFORMATION:  
; APPLICANT: LO, Kin-Ming  
; APPLICANT: Sun, Yaping  
; APPLICANT: Gillies, Stephen D.  
; TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as  
; TITLE OF INVENTION: FC Fusion Proteins  
; FILE REFERENCE: LEX-009  
; CURRENT APPLICATION NUMBER: US/09/977,034  
; PRIOR FILING DATE: 2001-10-11  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR FILING DATE: 1999-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 166  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Human IFN alpha-21 protein

US-09-977-034-19

Query Match 100.0%; Score 42; DB 5; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.067;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSK 8  
| | | | | | | |  
Db 131 LTERKYSK 138

## RESULT 9

US-09-633-516B-13  
; Sequence 13, Application US/09633516B  
; GENERAL INFORMATION:  
; APPLICANT: Francis Joseph CARR  
; APPLICANT: Fiona Suzanne ADAIR  
; APPLICANT: Anita Anne HAMILTON  
; APPLICANT: Graham CARTER  
; TITLE OF INVENTION: Modifying Protein Immunogenicity  
; TITLE OF INVENTION: 112408-120  
; FILE REFERENCE: 112408-120  
; CURRENT APPLICATION NUMBER: US/09/633,516B  
; 2000-08-04  
; CURRENT FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: PCT/GB99/04119  
; PRIOR FILING DATE: 1999-12-08  
; PRIOR APPLICATION NUMBER: GB9826925.1  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: GB9902139.6  
; PRIOR FILING DATE: 1999-02-02  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 165  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: US-09-633-516B-13

Query Match 85.7%; Score 36; DB 5; Length 165;  
Best Local Similarity 87.5%; Pred. No. 1.1;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERKYSK 8  
| | | | | | | |  
Db 130 LTERKYSK 137

## RESULT 10

US-09-633-516B-14  
; Sequence 14, Application US/09633516B  
; GENERAL INFORMATION:  
; APPLICANT: Francis Joseph CARR  
; APPLICANT: Fiona Suzanne ADAIR  
; APPLICANT: Anita Anne HAMILTON  
; APPLICANT: Graham CARTER  
; TITLE OF INVENTION: Modifying Protein Immunogenicity  
; TITLE OF INVENTION: 112408-120  
; FILE REFERENCE: 112408-120  
; CURRENT APPLICATION NUMBER: US/09/633,516B  
; 2000-08-04  
; CURRENT FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: PCT/GB99/04119  
; PRIOR FILING DATE: 1999-12-08  
; PRIOR APPLICATION NUMBER: GB9826925.1  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: GB9902139.6  
; PRIOR FILING DATE: 1999-02-02  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 165  
; TYPE: PRT

ORGANISM: Homo sapiens  
US-09-633-516B-14

Query Match 85.7%; Score 36; DB 5; Length 165;  
Best Local Similarity 87.5%; Pred. No. 1.1;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTKKYSK 8  
| | | | |  
DB 130 LKCKYSK 137

RESULT 11  
US-09-977-034-9  
; Sequence 9, Application US/09977034  
; GENERAL INFORMATION:  
; APPLICANT: Lo, Kin-Ming  
; APPLICANT: Sun, Yaping  
; APPLICANT: Gillies, Stephen D.  
; TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as  
; FILE REFERENCE: LEX-009  
; CURRENT APPLICATION NUMBER: US/09/977,034  
; PRIOR FILING DATE: 2001-10-11  
; PRIOR APPLICATION NUMBER: US/09/575,503  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: US 60/134,895  
; PRIOR FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 165  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Human IFN alpha-2 protein  
US-09-977-034-9

Query Match 85.7%; Score 36; DB 5; Length 165;  
Best Local Similarity 87.5%; Pred. No. 1.1;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTKKYSK 8  
| | | | |  
DB 130 LKCKYSK 137

RESULT 12  
US-09-977-034-13  
; Sequence 13, Application US/09977034  
; GENERAL INFORMATION:  
; APPLICANT: Lo, Kin-Ming  
; APPLICANT: Sun, Yaping  
; APPLICANT: Gillies, Stephen D.  
; TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as  
; FILE REFERENCE: LEX-009  
; CURRENT APPLICATION NUMBER: US/09/977,034  
; PRIOR FILING DATE: 2001-10-11  
; PRIOR APPLICATION NUMBER: US/09/575,503  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: US 60/134,895  
; PRIOR FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 166  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Human IFN alpha-7 protein

US-09-977-034-13

Query Match 85.7%; Score 36; DB 5; Length 166;  
Best Local Similarity 87.5%; Pred. No. 1.1;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTKKYSK 8  
| | | | |  
DB 131 LMKKYSK 138

RESULT 13  
US-09-977-034-16  
; Sequence 16, Application US/09977034  
; GENERAL INFORMATION:  
; APPLICANT: Lo, Kin-Ming  
; APPLICANT: Sun, Yaping  
; APPLICANT: Gillies, Stephen D.  
; TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as  
; FILE REFERENCE: LEX-009  
; CURRENT APPLICATION NUMBER: US/09/977,034  
; PRIOR FILING DATE: 2001-10-11  
; PRIOR APPLICATION NUMBER: US/09/575,503  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: US 60/134,895  
; PRIOR FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Human IFN alpha-14 protein  
US-09-977-034-16

Query Match 85.7%; Score 36; DB 5; Length 170;  
Best Local Similarity 87.5%; Pred. No. 1.1;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTKKYSK 8  
| | | | |  
DB 135 LMKKYSK 142

RESULT 14  
US-60-329-756-2  
; Sequence 2, Application US/60329756  
; GENERAL INFORMATION:  
; APPLICANT: COR Therapeutics, Inc.  
; APPLICANT: Tomlinson, James E.  
; TITLE OF INVENTION: VLP2 Gene and Protein  
; FILE REFERENCE: 044481-5087-PR  
; CURRENT APPLICATION NUMBER: US/60/329,756  
; CURRENT FILING DATE: 2001-10-18  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 831  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-329-756-2

Query Match 85.7%; Score 36; DB 6; Length 831;  
Best Local Similarity 75.0%; Pred. No. 6;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTKKYSK 8  
: | | | | |

Db 590 VTERKYS 697

RESULT 15  
US-09-977-034-14  
; Sequence 14, Application US/09977034  
; GENERAL INFORMATION:  
; APPLICANT: LO, Kin-Ming  
; APPLICANT: Sun, Yaping  
; APPLICANT: Gillies, Stephen D.  
; TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as  
; FILE REFERENCE: LEX-009  
; CURRENT APPLICATION NUMBER: US/09/977,034  
; CURRENT FILING DATE: 2001-10-11  
; PRIOR APPLICATION NUMBER: US/09/575,503  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: US 60/134,895  
; PRIOR FILING DATE: 1999-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 166  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Human IFN alpha-8 protein  
US-09-977-034-14

Query Match 83.3%; Score 35; DB 5; Length 166;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTERKYS 7  
Db 131 LTERKYS 137

Search completed: December 13, 2001, 10:49:47  
Job time: 307 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.  
OM protein - protein search, using sw model  
Run on: December 13, 2001, 10:44:40 ; Search time 19.94 Seconds  
(without alignments)  
9.028 Million cell updates/sec

Title: US-09-424-080A-1  
Perfect score: 42  
Sequence: 1 LTERKYSF 8  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /cgn2.6/ptodata/2/iaa/5A-COMB.pep.\*  
2: /cgn2.6/ptodata/2/iaa/5B-COMB.pep.\*  
3: /cgn2.6/ptodata/2/iaa/5A-COMB.pep.\*  
4: /cgn2.6/ptodata/2/iaa/5B-COMB.pep.\*  
5: /cgn2.6/ptodata/2/iaa/5A-COMB.pep.\*  
6: /cgn2.6/ptodata/2/iaa/5B-COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	8	2	US-08-669-284B-30
2	42	100.0	11	1	US-08-362-453-4
3	42	100.0	18	1	US-08-362-453-5
4	42	100.0	150	1	US-08-362-453-10
5	42	100.0	150	1	US-08-362-453-11
6	42	100.0	150	1	US-08-362-453-12
7	42	100.0	162	1	US-08-362-453-13
8	42	100.0	165	1	US-08-362-453-14
9	42	100.0	165	1	US-08-362-453-14
10	42	100.0	166	1	US-08-362-453-8
11	42	100.0	166	1	US-08-362-453-9
12	42	100.0	166	2	US-08-489-066A-16
13	42	100.0	166	3	US-08-819-236A-16
14	42	100.0	166	3	US-08-819-236A-2
15	42	100.0	166	4	US-08-954-395A-9
16	42	100.0	166	4	US-08-954-395A-10
17	42	100.0	166	4	US-08-954-395A-11
18	42	100.0	166	4	US-08-954-395A-12
19	42	100.0	166	4	US-08-954-395A-13
20	42	100.0	166	4	US-08-954-395A-14
21	42	100.0	166	4	US-08-954-395A-15
22	42	100.0	166	4	US-08-954-395A-16
23	42	100.0	166	4	US-08-954-395A-17
24	42	100.0	166	4	US-08-489-071A-16
25	42	100.0	166	4	US-08-339-913B-75
26	42	100.0	166	4	US-09-339-913B-76
27	42	100.0	166	4	US-09-339-913B-77

28	42	100.0	166	4	US-09-339-913B-79
29	42	100.0	166	4	US-09-339-913B-80
30	42	100.0	166	4	US-09-339-913B-81
31	42	100.0	166	4	US-09-339-913B-82
32	42	100.0	166	4	US-09-339-913B-83
33	42	100.0	189	1	US-08-026-758-1
34	42	100.0	189	1	US-08-026-758-2
35	42	100.0	189	1	US-08-026-758-3
36	42	100.0	189	1	US-08-026-758-6
37	42	100.0	189	1	US-08-026-758-7
38	42	100.0	189	1	US-08-026-758-11
39	42	100.0	189	1	US-08-026-758-16
40	42	100.0	189	1	US-08-026-758-17
41	42	100.0	189	1	US-08-026-758-19
42	42	100.0	189	1	US-08-026-758-20
43	42	100.0	189	2	US-08-489-066A-2
44	42	100.0	189	3	US-08-489-072A-2
45	42	100.0	189	4	US-09-206-935-8

## ALIGNMENTS

RESULT 1  
US-08-669-284B-30  
Sequence 30, Application US/08669284B  
Patent No. 5939534  
GENERAL INFORMATION:  
APPLICANT: Inoue, Makoto  
APPLICANT: Kikuchi, Kaoru  
APPLICANT: Ishige, Yoko  
APPLICANT: Ito, Akira  
APPLICANT: Kimura, Toru  
APPLICANT: Nakamura, Chikao  
APPLICANT: No. 5939534uchl, Hiroshi  
TITLE OF INVENTION: NOVEL HUMAN CILIARY NEUTROTROPIC FACTORS  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: SUGHRUE, MIOM, ZINN, MACPEAK & SEAS  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/669,284B  
FILING DATE: 28-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP94/02269  
FILING DATE: 27-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 06-268281  
FILING DATE: 05-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 06-201504  
FILING DATE: 03-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 05-350934  
FILING DATE: 29-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Nakamura, Dean H.  
REGISTRATION NUMBER: 33,981  
REFERENCE/DOCKET INFORMATION: Q-42041  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:

Sequence 79, Appl
Sequence 80, Appl
Sequence 83, Appl
Sequence 84, Appl
Sequence 85, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 6, Appl
Sequence 7, Appl
Sequence 11, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 19, Appl
Sequence 20, Appl
Sequence 2, Appl
Sequence 8, Appl

LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: 11near  
MOLECULE TYPE: peptide  
US-08-669-284B-30

Query Match 100.0% Score 42; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSY 8  
DB 1 LTERKYSY 8

RESULT 2  
US-08-362-453-4  
Sequence 4, Application US/08362453  
Patent No. 5684129  
GENERAL INFORMATION:  
APPLICANT: FISH, Eleanor N.  
TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/08/362.453  
FILING DATE: 06-JAN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/909,739  
FILING DATE: 07-JUL-1992  
APPLICATION NUMBER: US 07/980,525  
FILING DATE: 20-NOV-1992  
APPLICATION NUMBER: PCT/CA93/00279  
FILING DATE: 06-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitts, Monica Chin  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P638-4017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 4:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-362-453-4

Query Match 100.0% Score 42; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0064;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSY 8  
DB 2 LTERKYSY 9

RESULT 3  
US-08-362-453-5  
Sequence 5, Application US/08362453  
Patent No. 5684129  
GENERAL INFORMATION:  
APPLICANT: FISH, Eleanor N.  
TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/08/362.453  
FILING DATE: 06-JAN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/909,739  
FILING DATE: 07-JUL-1992  
APPLICATION NUMBER: US 07/980,525  
FILING DATE: 20-NOV-1992  
APPLICATION NUMBER: PCT/CA93/00279  
FILING DATE: 06-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitts, Monica Chin  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P638-4017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 5:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-362-453-5

Query Match 100.0% Score 42; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYSY 8  
DB 9 LTERKYSY 16

RESULT 4  
US-08-362-453-10  
Sequence 10, Application US/08362453  
Patent No. 5684129  
GENERAL INFORMATION:  
APPLICANT: FISH, Eleanor N.  
TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/362,453  
FILING DATE: 06-JAN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/909,739  
FILING DATE: 07-JUL-1992  
APPLICATION NUMBER: US 07/980,525  
FILING DATE: 20-NOV-1992  
APPLICATION NUMBER: PCT/CA93/00279  
FILING DATE: 06-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitts, Monica Chin  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P638-4017  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-362-453-10

Query Match 100.0%; Score 42; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYP 8  
Db 126 LTERKYP 133

RESULT 5  
US-08-362-453-11  
Sequence 11, Application US/08362453  
Patent No. 5684129  
GENERAL INFORMATION:  
APPLICANT: FISH, Eleanor N.  
TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/362,453  
FILING DATE: 06-JAN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/909,739  
FILING DATE: 07-JUL-1992  
APPLICATION NUMBER: US 07/980,525  
FILING DATE: 20-NOV-1992  
APPLICATION NUMBER: PCT/CA93/00279  
FILING DATE: 06-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitts, Monica Chin  
REGISTRATION NUMBER: 36,105

REFERENCE/DOCKET NUMBER: P638-4017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-362-453-11

Query Match 100.0%; Score 42; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERKYP 8  
Db 126 LTERKYP 133

RESULT 6  
US-08-362-453-12  
Sequence 12, Application US/08362453  
Patent No. 5684129  
GENERAL INFORMATION:  
APPLICANT: FISH, Eleanor N.  
TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/362,453  
FILING DATE: 06-JAN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/909,739  
FILING DATE: 07-JUL-1992  
APPLICATION NUMBER: US 07/980,525  
FILING DATE: 20-NOV-1992  
APPLICATION NUMBER: PCT/CA93/00279  
FILING DATE: 06-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitts, Monica Chin  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P638-4017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-362-453-12

Query Match 100.0%; Score 42; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LTERKYSKP 8
Db      126 LTERKYSKP 133

RESULT 7
US-08-362-453-15
; Sequence 15, Application US/08362453
; Patent No. 5684129
; GENERAL INFORMATION:
; APPLICANT: FISH, Eleanor N.
; TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,453
; FILING DATE: 06-JAN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/909,739
; FILING DATE: 07-JUL-1992
; APPLICATION NUMBER: US 07/980,525
; FILING DATE: 20-NOV-1992
; APPLICATION NUMBER: PCT/CA93/00279
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitts, Monica Chin
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P638-4017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-362-453-15

Query Match      100.0%; Score 42; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 LTERKYSKP 8
Db      127 LTERKYSKP 134

RESULT 8
US-08-362-453-13
; Sequence 13, Application US/08362453
; Patent No. 5684129
; GENERAL INFORMATION:
; APPLICANT: FISH, Eleanor N.
; TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington

```

```

STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,453
FILING DATE: 06-JAN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/909,739
FILING DATE: 07-JUL-1992
APPLICATION NUMBER: US 07/980,525
FILING DATE: 20-NOV-1992
APPLICATION NUMBER: PCT/CA93/00279
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kitts, Monica Chin
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P638-4017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-4810
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-362-453-13

Query Match      100.0%; Score 42; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 LTERKYSKP 8
Db      130 LTERKYSKP 137

RESULT 9
US-08-362-453-14
; Sequence 14, Application US/08362453
; Patent No. 5684129
; GENERAL INFORMATION:
; APPLICANT: FISH, Eleanor N.
; TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,453
; FILING DATE: 06-JAN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/909,739
; FILING DATE: 07-JUL-1992
; APPLICATION NUMBER: US 07/980,525
; FILING DATE: 20-NOV-1992
; APPLICATION NUMBER: PCT/CA93/00279
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitts, Monica Chin
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P638-4017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-362-453-13

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APPLICATION NUMBER: PCT/CA93/00279  
ATTORNEY/AGENT INFORMATION: FILING DATE: 06-JUL-1993  
NAME: Kitts, Monica Chin  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P638-4017  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-362-453-14

Query Match 100.0%; Score 42; DB 1; Length 165;  
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0;  
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 1 LTERKYSY 8  
DB 130 LTERKYSY 137

RESULT 10  
US-08-362-453-8  
Sequence 8, Application US/08362453  
Patent No. 5684129  
GENERAL INFORMATION:  
APPLICANT: FISH, Eleanor N.  
TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Nikola, Marmelstein, Murray & Oram  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 06-JAN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/909,739  
FILING DATE: 07-JUL-1992  
APPLICATION NUMBER: US 07/980,525  
FILING DATE: 20-NOV-1992  
APPLICATION NUMBER: PCT/CA93/00279  
FILING DATE: 06-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitts, Monica Chin  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P638-4017  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-362-453-8

Query Match 100.0%; Score 42; DB 1; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0;  
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 1 LTERKYSY 8  
DB 131 LTERKYSY 138

RESULT 11  
US-08-362-453-9  
Sequence 9, Application US/08362453  
Patent No. 5684129  
GENERAL INFORMATION:  
APPLICANT: FISH, Eleanor N.  
TITLE OF INVENTION: INTERFERON RECEPTOR BINDING PEPTIDES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Nikola, Marmelstein, Murray & Oram  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 06-JAN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/909,739  
FILING DATE: 07-JUL-1992  
APPLICATION NUMBER: US 07/980,525  
FILING DATE: 20-NOV-1992  
APPLICATION NUMBER: PCT/CA93/00279  
FILING DATE: 06-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitts, Monica Chin  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P638-4017  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-362-453-9

Query Match 100.0%; Score 42; DB 1; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0;  
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 1 LTERKYSY 8  
DB 131 LTERKYSY 138

RESULT 12  
US-08-489-066A-16  
Sequence 16, Application US/08489066A  
Patent No. 5869293  
GENERAL INFORMATION:  
APPLICANT: PESTKA, SIDNEY  
TITLE OF INVENTION: SUPER PROTEINS INCLUDING INTERFERONS,  
US-08-489-066A-16

;; TITLE OF INVENTION: INTERLEUKINS, ET AL.

;; NUMBER OF SEQUENCES: 16

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Klauber & Jackson

;; STREET: 411 Hackensack Avenue

;; CITY: Hackensack

;; STATE: New Jersey

;; COUNTRY: USA

;; ZIP: 07601

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/489,066A

;; FILING DATE: 09-JUN-1995

;; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/257,784

;; FILING DATE: 10-JUN-1994

;; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/076,231

;; FILING DATE: 11-JUN-1993

;; CLASSIFICATION: 435

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Fehlnert, Ph.D., Esq., Paul F.

;; REGISTRATION NUMBER: 35,135

;; REFERENCE/DOCKET NUMBER: 1705-1-002 CIPC

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 201 487-5800

;; TELEFAX: 201 343-1684

;; TELEX: 133521

;; INFORMATION FOR SEQ ID NO: 16:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 166 amino acids

;; TYPE: amino acid

;; TOPOLOGY: unknown

;; MOLECULE TYPE: protein

;; HYPOTHETICAL: NO

;; IMMEDIATE SOURCE:

;; CLONE: Hu-IFN-alpha001

;; US-08-489-066A-16

Query Match 100.0%; Score 42; DB 2; Length 166;

Best Local Similarity 100.0%; Pred. No. 0.12;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTEKKYSP 8

Db 131 LTEKKYSP 138

RESULT 13

US-08-489-072A-16

; Sequence 16, Application US/08489072A

; Patent No. 6001389

; GENERAL INFORMATION:

; APPLICANT: PESTKA, SIDNEY

; TITLE OF INVENTION: SUPER PROTEINS INCLUDING INTERFERONS,

; INTERLEUKINS, ET AL.

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klauber & Jackson

; STREET: 411 Hackensack Avenue

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/489,072A

;; FILING DATE: 09-JUN-1995

;; CLASSIFICATION: 530

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/257,784

;; FILING DATE: 10-JUN-1994

;; CLASSIFICATION: 530

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/076,231

;; FILING DATE: 11-JUN-1993

;; CLASSIFICATION: 530

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Fehlnert, Ph.D., Esq., Paul F.

;; REGISTRATION NUMBER: 35,135

;; REFERENCE/DOCKET NUMBER: 1705-1-002 CIPA

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 201 487-5800

;; TELEFAX: 201 343-1684

;; TELEX: 133521

;; INFORMATION FOR SEQ ID NO: 16:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 166 amino acids

;; TYPE: amino acid

;; TOPOLOGY: unknown

;; MOLECULE TYPE: protein

;; HYPOTHETICAL: NO

;; IMMEDIATE SOURCE:

;; CLONE: Hu-IFN-alpha001

;; US-08-489-072A-16

Query Match 100.0%; Score 42; DB 3; Length 166;

Best Local Similarity 100.0%; Pred. No. 0.12;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTEKKYSP 8

Db 131 LTEKKYSP 138

RESULT 14

US-08-819-238A-2

; Sequence 2, Application US/08819238A

; Patent No. 6069133

; GENERAL INFORMATION:

; APPLICANT: Henry C. Chiu and Dennis J. Carlo

; TITLE OF INVENTION: TARGETED DELIVERY OF GENES ENCODING

; INTERFERON

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 60 STATE STREET, SUITE 510

; CITY: BOSTON

; STATE: MASSACHUSETTS

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/819,238A

; FILING DATE:

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/616,023

; FILING DATE: 14 MARCH 1996

; APPLICATION NUMBER: PCT/US96/

;; FILING DATE: 14 MARCH 1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: REMILLARD, JANE E.  
;; REGISTRATION NUMBER: 38,872  
;; REFERENCE/DOCKET NUMBER: TTI-143CPPC  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617)227-7400  
;; TELEFAX: (617)227-5941  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 166 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FRAGMENT TYPE: internal  
;; US-08-819-238A-2

Query Match 100.0%; Score 42; DB 3; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12; 0; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0; Mismatches 0; Gaps 0;

QY 1 LTEKKYSP 8  
Db 131 LTEKKYSP 138

## RESULT 15

US-08-954-395A-9  
; Sequence 9, Application US/08954395A  
; Patent No. 6204022  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Howard M.  
; APPLICANT: Subramaniam, Prem S.  
; APPLICANT: Pontzer, Carol H.  
; APPLICANT: Villarete, Lorelie H.  
; APPLICANT: Campos, Jackeline  
; APPLICANT: Chung, Albert D.  
; APPLICANT: Li, Wayne W.  
; APPLICANT: Liu, Philip T.  
; TITLE OF INVENTION: LOW-TOXICITY HUMAN INTERFERON-ALPHA  
; TITLE OF INVENTION: ANALOG  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Denlinger & Associates LLP  
; STREET: 350 Cambridge Ave., Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/954,395A  
; FILING DATE: Filed Herewith  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/631,328  
; FILING DATE: 12-APR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Denlinger, Peter J.  
; REGISTRATION NUMBER: 27008  
; REFERENCE/DOCKET NUMBER: 5600-0001.35  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-324-0880  
; TELEFAX: 650-324-0960  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 166 amino acids

;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; IMMEDIATE SOURCE:  
;; LIBRARY: GenBank Accessn. J00210, PID g386796  
;; CLONE: Human IFN alpha-d, mature protein  
;; US-08-954-395A-9

Query Match 100.0%; Score 42; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 0.12; 0; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0; Mismatches 0; Gaps 0;

QY 1 LTEKKYSP 8  
Db 131 LTEKKYSP 138

Search completed: December 13, 2001, 10:45:08  
Job time: 28 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 13, 2001, 11:55:37 ; Search time 22.27 Seconds  
(without alignments)  
27.364 Million cell updates/sec

Title: US-09-424-080A-1

Perfect score: 42

Sequence: 1 LTKKYSK 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 147

Minimum DB seq length: 8

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

--PIR\_68:--  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	50.0	8	2 S21663	neuropeptide - flo
2	18	42.9	8	2 S15422	adipokinetic hormo
3	18	42.9	8	2 A58841	adipokinetic hormo
4	17	40.5	8	2 A05169	neuropeptide M-I -
5	16	38.1	8	2 S20162	leghemoglobin III
6	16	38.1	8	2 A14683	aspartate transami
7	16	38.1	8	2 S45651	probable Na+-trans
8	14	33.3	8	2 A61348	red pigment-concen
9	14	33.3	8	2 S08995	hypertrehalosemic
10	14	33.3	8	2 A49823	adipokinetic hormo
11	14	33.3	8	2 A4960	neuropeptide Led-C
12	14	33.3	8	2 A43976	hypertrehalosemic
13	14	33.3	8	2 B43976	hypertrehalosemic
14	14	33.3	8	2 S11545	adipokinetic hormo
15	14	33.3	8	2 D47393	neuropeptide calla
16	12	28.6	8	2 S16324	hypothetical prote
17	12	28.6	8	2 A23967	leucoperoxin M
18	11	26.2	8	2 S08996	hypertrehalosemic
19	11	26.2	8	2 S10596	adipokinetic hormo
20	11	26.2	8	2 B49823	adipokinetic hormo
21	11	26.2	8	2 B49823	neuropeptide Led-C
22	11	26.2	8	2 A3995	adipokinetic hormo
23	11	26.2	8	2 S55310	adipokinetic hormo
24	11	26.2	8	2 A58620	adipokinetic hormo
25	11	26.2	8	2 S21273	cellulase (EC 3.2.
26	11	26.2	8	2 S21288	lectin - potato (f
27	11	26.2	8	2 JS0318	leucokinin VIII -
28	11	26.2	8	2 I57018	gene cfr protein
29	10	23.8	8	2 A32523	peptidyl-dipeptida

## ALIGNMENTS

### RESULT 1

S21663

neuropeptide - flower beetle (Pachnoda marginata)

C:Species: Pachnoda marginata

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997

C:Accession: S21663

R:Gaede, G.; Lopata, A.; Kellner, R.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 373, 133-142, 1992

A>Title: Primary structures of neuropeptides isolated from the corpora cardiaca of va  
ectrometry.

A:Reference number: S21663; MUID:92265187

A:Accession: S21663

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <GAE>

Query Match

Best Local Similarity 50.0%; Score 21; DB 2; Length 8;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKKYSP 8

DB 1 ELAYSP 6

### RESULT 2

S15422

adipokinetic hormone - cockchafer

C:Species: Melolontha melolontha (cockchafer)

C>Date: 19-Mar-1997 #sequence\_revision 31-Oct-1997 #text\_change 31-Oct-1997

C:Accession: S15422

R:Gaede, G.

Biochem. J. 275, 671-677, 1991

A>Title: A unique charged tyrosine-containing member of the adipokinetic hormone/ red

A:Reference number: S15422; MUID:91248100

A:Accession: S15422

A:Molecule type: protein

A:Residues: 1-8 <BIO>

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (c1n) #status experimental

F:8/Modified site: amidated carboxyl end (trp) #status experimental

Query Match

Best Local Similarity 42.9%; Score 18; DB 2; Length 8;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YSP 8

DB 4 YSP 6

```

RESULT 3
A58641
adipokine hormone - dor beetle
C:Species: Geotrupes stercorarius (dor beetle)
C>Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 31-Oct-1997
C:Accession: A58641
R:Gaede, G. 275, 671-677, 1991
A:Title: A unique charged tyrosine-containing member of the adipokine hormone/red-pigment concentrating hormone family
A:Reference number: S15422; MUID:91248100
A:Accession: A58641
A:Molecule type: protein
A:Residues: 1-8 <BIO>
C:Superfamily: adipokine hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 42.9%; Score 18; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YSP 8
Db 4 YSP 6

RESULT 4
A05169
neuropeptide M-I - American cockroach
C:Species: Periplaneta americana (American cockroach)
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Dec-1993
C:Accession: A05169
R:Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L.
Biochem. Biophys. Res. Commun. 124, 350-358, 1984
A:Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry
A:Reference number: A90118; MUID:85046530
A:Accession: A05169
A:Molecule type: protein
A:Residues: 1-8 <WTP>
C:Keywords: neuropeptide

Query Match 40.5%; Score 17; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKKYSP 8
Db 1 EVNFSF 6

RESULT 5
S20162
leghemoglobin III - Sesbania rostrata (fragment)
C:Species: Sesbania rostrata
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 04-Mar-2000
C:Accession: S20162
R:Metz, B.A.; Welters, P.; Hoffmann, H.J.; Jensen, E.O.; Schell, J.; de Bruijn, F.J.
Mol. Gen. Genet. 214, 181-191, 1988
A:Title: Primary structure and promoter analysis of leghemoglobin genes of the stem-nodule
A:Reference number: S08322; MUID:89181515
A:Accession: S20162
A:Molecule type: DNA
A:Residues: 1-8 <MET>
A:Cross-references: EMBL:X13504; NID:G21383; PIDN:CAA31058.1; PTD:G579482
C:Genetics:
A:Gene: glib
C:Superfamily: globin; globin homology
C:Keywords: heme; oxygen carrier

```

```

Query Match 38.1%; Score 16; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TEKK 5
Db 4 TEKQ 7

RESULT 6
A14683
aspartate transaminase (EC 2.6.1.1), mitochondrial - chicken (tentative sequence) (fr
N:Alternate names: aspartate aminotransferase, mitochondrial
C:Species: Gallus gallus (chicken)
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000
C:Accession: A14683
R:Wilson, K.J.; Hunziker, P.; Hughes, G.J.
FEBS Lett. 108, 98-102, 1979
A:Title: Microsequence analysis: IV. Automatic liquid-phase sequencing using DABITC.
A:Reference number: A14683; MUID:80092116
A:Accession: A14683
A:Molecule type: protein
A:Residues: 1-8 <WIL>
C:Keywords: aminotransferase; mitochondrion

Query Match 38.1%; Score 16; DB 2; Length 8;
Best Local Similarity 28.6%; Pred. No. 2.2e+05;
Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 TEKKYSP 8
Db 1 SENNFQ 7

RESULT 7
S45651
probable Na+-transporting ATP synthase (EC 3.6.1.-) - Acetobacterium woodii (fragment
C:Species: Acetobacterium woodii
C>Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 07-May-1999
C:Accession: S45651
R:Reidlinger, J.; Mueller, V.
Eur. J. Biochem. 223, 275-283, 1994
A:Title: Purification of ATP synthase from Acetobacterium woodii and identification a
A:Reference number: S45648; MUID:94307271
A:Accession: S45651
A:Molecule type: protein
A:Residues: 1-8 <REI>
A:Experimental source: DSM 1030
C:Keywords: hydrolase

Query Match 38.1%; Score 16; DB 2; Length 8;
Best Local Similarity 42.9%; Pred. No. 2.2e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LFEKKYS 7
Db 2 LVASKYA 8

RESULT 8
A61348
red pigment-concentrating hormone - northern shrimp
N:Alternate names: blanching hormone
C:Species: Pandalus borealis (northern shrimp)
C>Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
C:Accession: A61348; S07139
R:Fernlund, P.; Josefsson, L.
Science 177, 173-175, 1972
A:Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.

```

A:Reference number: A61348; MUID:72228738

A:Accession: A61348

A:Molecule type: protein

A:Residues: 1-8 <FER1>

R:Perlund, P.

Biochim. Biophys. Acta 371, 304-311, 1974

A:Title: Structure of the red-pigment-concentrating hormone of the shrimp, *Pandalus borealis*

A:Reference number: S07139; MUID:75054965

A:Accession: S07139

A:Molecule type: protein

A:Residues: 1-8 <PER2>

A:Note: The amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have

used pigment-containing cells.

C:Superfamily: adipo-kinetic hormone

C:Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutamate

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 33.3%; Score 14; DB 2; Length 8;

Best Local Similarity 66.7%; Pred. No. 2.2e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YSP 8

Db 4 FSP 6

RESULT 9

S08995

hypertrehalosemic hormone I - oriental cockroach

N:Alternate names: Pea-CAH-I

C:Species: *Blattella orientalis* (oriental cockroach)

C:Date: 30-Jun-1992 #sequence\_revision 24-Oct-1997 #text\_change 31-Oct-1997

C:Accession: S08995

R:Gaede, G.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A:Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora

allata and of the stick insect *Extatosoma tiaratum* assigned by tandem fast atom bombard

A:Reference number: S08995; MUID:90253659

A:Accession: S08995

A:Molecule type: protein

A:Residues: 1-8 <GAE>

A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have

used pigment-containing cells.

C:Superfamily: adipo-kinetic hormone

C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 33.3%; Score 14; DB 2; Length 8;

Best Local Similarity 66.7%; Pred. No. 2.2e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YSP 8

Db 4 FSP 6

RESULT 10

A49823

adipo-kinetic hormone I - American cockroach

N:Alternate names: periplanetin CC-1

C:Species: *Periplaneta americana* (American cockroach)

C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 07-May-1999

C:Accession: A49823

R:Scarborough, R.W.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller, C.

Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984

A:Title: Isolation and primary structure of two peptides with cardioacceleratory and hyp

A:Reference number: A49823; MUID:84298179

A:Accession: A49823

A:Molecule type: protein

A:Residues: 1-8 <SCA>

C:Superfamily: adipo-kinetic hormone

C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyrogluta

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 33.3%; Score 14; DB 2; Length 8;

Best Local Similarity 66.7%; Pred. No. 2.2e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YSP 8

Db 4 FSP 6

RESULT 11

A44960

neuropeptide Led-CC-I - Colorado potato beetle

C:Species: *Leptinotarsa decemlineata* (Colorado potato beetle)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C:Accession: A44960

R:Gaede, G.; Kellner, R.

Peptides 10, 1287-1289, 1989

A:Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle a

A:Reference number: A44960; MUID:90160053

A:Accession: A44960

A:Molecule type: protein

A:Residues: 1-8 <GAE>

C:Superfamily: adipo-kinetic hormone

C:Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutam

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimen

Query Match 33.3%; Score 14; DB 2; Length 8;

Best Local Similarity 66.7%; Pred. No. 2.2e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YSP 8

Db 4 FSP 6

RESULT 12

A43976

hypertrehalosemic hormone - yellow mealworm

C:Species: *Tenebrio molitor* (yellow mealworm)

C:Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 07-May-1999

C:Accession: A43976

R:Gaede, G.; Rosinski, G.

Peptides 11, 455-459, 1990

A:Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid

A:Reference number: A43976; MUID:90341081

A:Accession: A43976

A:Molecule type: protein

A:Residues: 1-8 <GAE>

C:Superfamily: adipo-kinetic hormone

C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyrogluta

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 33.3%; Score 14; DB 2; Length 8;

Best Local Similarity 66.7%; Pred. No. 2.2e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YSP 8

Db 4 FSP 6

RESULT 13

B43976  
 hypertrahalosemic hormone - beetle (Zophobas rugipes)  
 C:Species: Zophobas rugipes  
 C>Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 07-May-1999  
 C:Accession: B43976  
 R:Gaede, G.; Rosinski, G.  
 Peptides 11, 455-459, 1990  
 A:Title: The primary structure of the hypertrahalosemic neuropeptide from tenebrionid beetle  
 A:Reference number: A43976; MUID:90341081  
 A:Accession: B43976  
 A:Molecule type: protein  
 A:Residues: 1-8 <GAE>

C:Superfamily: adipokinetic hormone  
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:8/Modified site: amidated carboxyl end (trp) #status experimental

Query Match 33.3%; Score 14; DB 2; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 2.2e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 YSP 8  
 :||  
 DB 4 FSP 6

## RESULT 14

S11545  
 adipokinetic hormone - nestling-sucking blowfly  
 C:Species: Protophormia terraenovae (nestling-sucking blowfly)  
 C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 31-Oct-1997  
 C:Accession: S11545

R:Gaede, G.; Wilps, H.; Kellner, R.  
 Biochem. J. 269, 309-313, 1990  
 A:Title: Isolation and structure of a novel charged member of the red-pigment-concentrat  
 erraenovae (Diptera)  
 A:Reference number: S11545; MUID:90351345

A:Accession: S11545  
 A:Molecule type: protein  
 A:Residues: 1-8 <GAE>  
 C:Superfamily: adipokinetic hormone  
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:8/Modified site: amidated carboxyl end (trp) #status experimental

Query Match 33.3%; Score 14; DB 2; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 2.2e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 YSP 8  
 :||  
 DB 4 FSP 6

## RESULT 15

D47393  
 neuropeptide callatostatin 4 - bluebottle fly (Calliphora vomitoria)  
 C:Species: Calliphora vomitoria  
 C>Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 28-Apr-1995  
 C:Accession: D47393

R:Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993  
 A:Title: Callatostatins: neuropeptides from the blowfly Calliphora vomitoria with sequen  
 A:Reference number: A47393; MUID:93211980  
 A:Accession: D47393

A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-8 <DUV>  
 A:Experimental source: thoracic ganglia  
 A>Note: sequence extracted from NCBI backbone (NCBIP:128479)

Query Match 33.3%; Score 14; DB 2; Length 8;  
 Best Local Similarity 40.0%; Pred. No. 2.2e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 EKKYS 7  
 :||  
 DB 1 DRPYS 5

Search completed: December 13, 2001, 11:56:34  
 Job time: 57 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 13, 2001, 11:56:37 ; Search time 12.48 Seconds  
(without alignments)  
23.503 Million cell updates/sec

Title: US-09-424-080a-1

Perfect score: 42

Sequence: qd-1TEKKYSP:8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 64

Minimum-DB seq length: 8

Maximum-DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	45.2	8	1 UH09_RAT	P56575 rattus norv
2	18	42.9	8	1 AKH_MEML	P25423 melolontha
3	14	33.3	8	1 ALL4_CALVO	P41840 calliphora
4	14	33.3	8	1 HTF1_PERAM	P04548 periplaneta
5	14	33.3	8	1 HTF1_TENNO	P25419 tenebrio mo
6	14	33.3	8	1 RPKH_PANBO	P08939 panalio bo
7	13	31.0	8	1 LMT2_LOCOMI	P22396 locusta nig
8	12	28.6	8	1 ALL7_CARMA	P81820 carcinus ma
9	12	28.6	8	1 ALL4_CVDPO	P82154 cydia pomon
10	12	28.6	8	1 ALL4_CVDPO	P82155 cydia pomon
11	12	28.6	8	1 LPK_LEUMA	P13049 leucophaea
12	11	26.2	8	1 AKH_LIBAU	P25418 libellula a
13	11	26.2	8	1 AKH_TABAT	P14595 tabanus atr
14	11	26.2	8	1 ALL5_CARMA	P81818 carcinus ma
15	11	26.2	8	1 ALL6_CARMA	P81821 carcinus ma
16	11	26.2	8	1 ALL8_CVDPO	P82152 cydia pomon
17	11	26.2	8	1 ALL7_CVDPO	P81809 carcinus ma
18	11	26.2	8	1 HTF2_PERAM	P04549 periplaneta
19	11	26.2	8	1 LCK8_LEUMA	P19950 leucophaea
20	11	26.2	8	1 PKK2_PERAM	P82692 periplaneta
21	10	23.8	8	1 FARK_HOMAM	P41487 homarus ame
22	10	23.8	8	1 NPB_BOVIN	P15507 bos taurus
23	9	21.4	8	1 ACI_THUAL	P18691 thunnus alb
24	9	21.4	8	1 ANG2_BOTJA	Q10582 bothrops ja
25	9	21.4	8	1 B44K_PORGI	P81886 porphyromon
26	9	21.4	8	1 UPAA_HUMAN	P30096 homo sapien
27	9	21.4	8	1 ALL6_CARMA	P81815 carcinus ma
28	8	19.0	8	1 ALL2_CVDPO	P82157 cydia pomon
29	8	19.0	8	1 ALL8_CARMA	P81812 carcinus ma
30	8	19.0	8	1 ALL9_CARMA	P81811 carcinus ma
31	8	19.0	8	1 CLP_THICU	P80488 thibacillu
32	8	19.0	8	1 FAR3_HOMAM	P41486 homarus ame
33	8	19.0	8	1 FAR3_HOMAM	P41486 homarus ame

34	8	19.0	8	1 RS7_MYCIT	P33564 mycobacteri
35	7	16.7	8	1 ACT_CARMA	P80709 carcinus ma
36	7	16.7	8	1 AKHG_GRTBI	P14086 gryllus bim
37	7	16.7	8	1 ALL5_CALVO	P41841 calliphora
38	7	16.7	8	1 ALL5_CVDPO	P82156 cydia pomon
39	7	16.7	8	1 CAD1_ENTFA	P13268 enterococcu
40	7	16.7	8	1 CCKN_MACEU	P30369 macropus eu
41	7	16.7	8	1 FAR1_PANRE	P41872 panagrellus
42	7	16.7	8	1 FAR7_ASCSU	P43171 ascaris suu
43	7	16.7	8	1 FUSS_FUSSO	P81010 fusarium so
44	7	16.7	8	1 GLUR_HUMAN	P02729 homo sapien
45	7	16.7	8	1 LCK1_LEUMA	P21140 leucophaea

## ALIGNMENTS

RESULT 1	UH09_RAT	STANDARD	PRT	8 AA
ID	P56575			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	UNKNOWN PROTEIN FROM 2D-PAGE OF HEART TISSUE (SPOT P9) (FRAGMENT).			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE.			
RC	STRAIN=WISTAR; TISSUE=Heart;			
RA	Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,			
RA	Jungblut P.R.;			
RL	Submitted (SEP-1998) to the SWISS-PROT data bank.			
CC	-1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN			
CC	PROTEIN IS: 8.9, ITS MW IS: 42 KDA.			
FT	NON_TER 8			
SQ	SEQUENCE 8 AA; 1029 MW; 9E0775A6C4140B06 CRC64;			

Query Match 45.2%; Score 19; DB 1; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY	3	EKKYSP 8
DB	2	ERRQSP 7

RESULT 2	AKH_MEML	STANDARD	PRT	8 AA
ID	P25423			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	01-FEB-1994 (Rel. 28, Last annotation update)			
DE	ADIPOKINETIC HORMONE (AKH).			
OS	Melolontha melolontha (Cockchafer),			
OS	Geotrupes stercorosus (Dor beetle), and			
OS	Pachnoda marginata (Flower beetle).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;			
OC	Scarabaeiformia; Scarabaeidae; Melolonthinae;			
OC	NCBI_TaxID=7061, 7087, 7058;			
RN	[1]			
RP	SEQUENCE.			
RC	SPECIES=M.melolontha, and G.stercorosus; TISSUE=Corpora cardiaca;			
RC	MEDLINE=91248100; PubMed=2039445;			
RA	Gaede G.;			
RT	"A unique charged tyrosine-containing member of the adipokinetic			
RT	hormone/red-pigment-concentrating hormone peptide family isolated and			
RT	sequenced from two beetle species."			



RL Blochem. J. 275:671-677(1991).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES-P. marginata; TISSUE-Corpora cardiaca;  
 RX MEDLINE-92265187; PubMed-1586453;  
 RA Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;  
 RT "Primary structures of neuropeptides isolated from the corpora  
 RT cardiaca of various cetonid beetle species determined by  
 RT pulsed-liquid phase sequencing and tandem fast atom bombardment mass  
 RT spectrometry.";  
 RL Biol. Chem. Hoppe-Seyler 373:133-142(1992).  
 CC -1- FUNCTION: THIS HORMONE RELEASED FROM CELLS IN THE CORPORA  
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF  
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT  
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.  
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
 DR PIR; S13422; S13422.  
 DR PIR; S21663; S21663.  
 DR INTERPRO; IPR002047; AKH.  
 DR PROSITE; PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Flight.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 1022 MW; 867AB775AB544736 CRC64;  
  
 Query Match 42.9%; Score 18; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1e+05; 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 6 YSP 8  
 DB 4 YSP 6  
  
 RESULT 3  
 ID ALL4.CALVO STANDARD; PRT; 8 AA.  
 AC P41840;  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE CALLATOSTATIN 4 (LEU-CALLATOSTATIN 4).  
 OS Calliphora vomitoria (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Oestroidea; Calliphoridae; Calliphora.  
 OX NCBI\_TaxID=27454;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-Thoracic ganglion;  
 RX MEDLINE-93211980; PubMed-8460157;  
 RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,  
 RA Thorpe A.;  
 RT "Callatostatin: neuropeptides from the blowfly Calliphora vomitoria  
 RT with sequence homology to cockroach allatostatins.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).  
 RN [2]  
 RP CHARACTERIZATION.  
 RX MEDLINE-94291167; PubMed-8020069;  
 RA Duve H., Thorpe A.;  
 RT "Distribution and functional significance of Leu-callatostatins in  
 RT the blowfly Calliphora vomitoria.";  
 RL Cell Tissue Res. 276:367-379(1994).  
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY  
 CC A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE  
 CC INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO  
 CC BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO  
 CC FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.  
 CC -1- TISSUE SPECIFICITY: BRAIN, SUBESOPHAGEAL GANGLION, RETROCEBRAL  
 CC COMPLEX, THORACICO-ABDOMINAL GANGLION, PERIPHERAL NEUROSECRETORY  
 CC SYSTEM AND INTESTINE.  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.

DR PIR; D47393; D47393.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 FT UNSURE 1 1 OR N.  
 SQ SEQUENCE 8 AA; 954 MW; D32879D5AB47740A CRC64;  
  
 Query Match 33.3%; Score 14; DB 1; Length 8;  
 Best Local Similarity 40.0%; Pred. No. 1e+05; 1; Indels 0; Gaps 0;  
 Matches 2; Conservative 2; Mismatches 2;  
  
 QY 3 EKKYS 7  
 DB 1 DRPYS 5  
  
 RESULT 4  
 ID HTFL.PEAM STANDARD; PRT; 8 AA.  
 AC P04548;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE HYPERTREHALOSAEMIC FACTOR I (NEUROPEPTIDE M-I) (PERIPLANETIN CC-I)  
 DE (PEA-CAH-I) (LED-CC-I) (HYPERTREHALOSAEMIC NEUROPEPTIDE I).  
 OS Periplaneta americana (American cockroach).  
 OS Leptinotarsa decemlineata (Colorado potato beetle), and  
 OS Blattella orientalis (Oriental cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;  
 OC Blattodea; Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978; 7539, 6976;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES-P. americana;  
 RX MEDLINE-95046530; PubMed-6548628;  
 RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,  
 RA Rinehart K.L. Jr.;  
 RT "Structures of two cockroach neuropeptides assigned by fast atom  
 RT bombardment mass spectrometry.";  
 RL Biochem. Biophys. Res. Commun. 124:350-358(1984).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES-P. americana;  
 RX MEDLINE-84298179; PubMed-6591205;  
 RA Scarborough R.M., Jameson G.C., Kalish F., Kramer S.J., McEnroe G.A.,  
 RA Miller C.A., Schooley D.A.;  
 RT "Isolation and primary structure of two peptides with  
 RT cardioacceleratory and hyperglycemic activity from the corpora  
 RT cardiaca of Periplaneta americana.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).  
 RN [3]  
 RP SEQUENCE.  
 RC SPECIES-L. decemlineata; TISSUE-Corpora cardiaca;  
 RX MEDLINE-90160053; PubMed-2576128;  
 RA Gaede G., Kellner R.;  
 RT "The metabolic neuropeptides of the corpus cardiaca from the potato  
 RT beetle and the American cockroach are identical.";  
 RL Peptides 10:1287-1289(1989).  
 RN [4]  
 RP SEQUENCE.  
 RC SPECIES-B. orientalis; TISSUE-Corpora cardiaca;  
 RX MEDLINE-90253659; PubMed-2340112;  
 RA Gaede G., Rinehart K.L. Jr.;  
 RT "Primary structures of hypertrehalosaemic neuropeptides isolated from  
 RT the corpora cardiaca of the cockroaches Leucophaea maderae, orientalis  
 RT Gromphodrhina portoricensis, Blattella germanica and Blattella orientalis  
 RT and of the stick insect Extatosoma tiaratum assigned by tandem fast  
 RT atom bombardment mass spectrometry.";  
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).  
 CC -1- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT  
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS  
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).

CC -1- SIMILARITY: BELONGS TO THE AKH / HRTX / RPCH FAMILY.  
 DE PIR; A05169; A05169.  
 DR PIR; S08995; S08995.  
 DR PIR; A49823; A49823.  
 DR PIR; A44960; A44960.  
 DR InterPro; IPR002047; AKH.  
 DR PROSITE; PS00256; AKH; 1.  
 DR Neuropeptide; Amidation.  
 FT MOD\_RES 1 1  
 FT MOD\_RES 8 8  
 FT AMIDATION  
 SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;

Query Match 33.3%; Score 14; DB 1; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1e+05; 0; Indels 0; Gaps 0;  
 Matches 2; Conservative 1; Mismatches 0; Gaps 0;

QY 6 YSP 8  
 DB 4 FSP 6

## RESULT 5

HTE\_TENMO STANDARD; PRT; 8 AA.  
 AC P25419;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE HYPERTREHALOSEMIC FACTOR (HOTH) (HYPERTREHALOSEMIC NEUROPEPTIDE).  
 OS Tenebrio molitor (Yellow mealworm), and Zophobas rugipes.  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;  
 OC Cucujiformia; Tenebrionidae; Tenebrio.  
 OX NCBI\_TaxID=7067, 7075;  
 RN [1]  
 RP SEQUENCE.

TISSUE=Corpora cardiaca;  
 RC MEDLINE=90341081; PubMed=2381871;  
 RA Gaede G., Rosinski G.;  
 RT "The primary structure of the hypertrehalosemic neuropeptide from  
 RT tenebrionid beetles: a novel member of the AKH/RPCH family.";  
 RL Peptides 11:435-439(1990).  
 CC -1- FUNCTION: HYPERTREHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT  
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS  
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).  
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTX / RPCH FAMILY.  
 DE PIR; A43976; A43976.  
 DR PIR; B43976; B43976.  
 DR InterPro; IPR002047; AKH.  
 DR PROSITE; PS00256; AKH; 1.  
 DR Neuropeptide; Amidation.  
 FT MOD\_RES 1 1  
 FT MOD\_RES 8 8  
 FT AMIDATION.  
 SQ SEQUENCE 8 AA; 1005 MW; 86745775B9C44736 CRC64;

Query Match 33.3%; Score 14; DB 1; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 YSP 8  
 DB 4 FSP 6

## RESULT 6

RPCH\_PANBO STANDARD; PRT; 8 AA.  
 AC P08939;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE RED PIGMENT CONCENTRATING HORMONE (RPCH).  
 OS Pandanus borealis (Northern red shrimp).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea; Pandaloidea;  
 OC Pandallidae; Pandalus.  
 OX NCBI\_TaxID=6703;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=75054965; PubMed=4433569;  
 RA Fernlund P.;  
 RT "Structure of the red-pigment-concentrating hormone of the shrimp,  
 RT Pandanus borealis.";  
 RL Biochim. Biophys. Acta 371:304-311(1974).  
 CC -1- FUNCTION: THIS HORMONE ADAPTS THE ANIMAL TO LIGHT BACKGROUNDS BY  
 CC -1- STIMULATING CONCENTRATION OF THE PIGMENT OF ITS RED BODY-  
 CC CHROMATOPHORES.  
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTX / RPCH FAMILY.  
 DE PIR; S07139; S07139.  
 DR InterPro; IPR002047; AKH.  
 DR PROSITE; PS00256; AKH; 1.  
 DR Pigment; Hormone; Amidation.  
 FT MOD\_RES 1 1  
 FT MOD\_RES 8 8  
 FT PYRROLIDONE CARBOXYLIC ACID.  
 FT AMIDATION.  
 SQ SEQUENCE 8 AA; 948 MW; 86786775B9C44736 CRC64;

Query Match 33.3%; Score 14; DB 1; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1e+05; 0; Indels 0; Gaps 0;  
 Matches 2; Conservative 1; Mismatches 0; Gaps 0;

QY 6 YSP 8  
 DB 4 FSP 6

## RESULT 7

LMT2\_LOCMI STANDARD; PRT; 8 AA.  
 AC P22396;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-AUG-1991 (Rel. 19, Last annotation update)  
 DE LOCUSTAMYTROPIN 2 (LOM-MT-2).  
 OS Locusta migratoria (Migratory locust).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;  
 OC Acridomorpha; Acridoidea; Acrididae; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.

TISSUE=Corpora cardiaca;  
 RC Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;  
 RT "Isolation, identification and synthesis of locustamytropin II, an  
 RT additional neurotrophic peptide of Locusta migratoria. Member of the  
 RT cephalomytropic peptide family.";  
 RL Insect Biochem. 20:479-484(1990).  
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC (MYOTROPIC ACTIVITY).  
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.

DE InterPro; IPR001484; PYROKININ.  
 DR PROSITE; PS00539; PYROKININ; 1.  
 DR Neuropeptide; Amidation; Pyrokinin.  
 FT MOD\_RES 8 8  
 FT AMIDATION.  
 SQ SEQUENCE 8 AA; 934 MW; 26341171A9CAA87B CRC64;

Query Match 31.0%; Score 13; DB 1; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1e+05;  
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKKYSP 8  
 DB 1 EGDFTP 6



CC PENTAPEPTIDE FRAGMENT FTPL.  
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 DR PIR: A23967; A23967;  
 DR InterPro: IPR001484; Pyrokinin.  
 DR PROSITE: PS00539; PYROKININ;  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 949 MW; 92341771A9D5A1B6 CRC64;

Query Match 28.6%; Score 12; DB 1; Length 8;  
 Best Local Similarity 16.7%; Pred. No. 1e+05;  
 Matches 1; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKKYSP 8  
 DB 1 QTSFTP 6

RESULT 12  
 AKH\_LIBAU STANDARD; PRT; 8 AA.  
 AC P25418;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE ADIPOKINETIC HORMONE (AKH).  
 OS Libellula auripennis (Skimmer dragonfly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.  
 OX NCBI\_TaxID=6966;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE-Corpora cardiaca;  
 RX MEDLINE=90359055; PubMed=2390213;  
 GA Gaede G.;  
 RA "The putative ancestral peptide of the adipokinetic/red-pigment-  
 RT concentrating hormone family isolated and sequenced from a  
 RL dragonfly.";  
 RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).  
 CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA  
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF  
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT  
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.  
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
 CC PIR: S10596; S10596;  
 DR InterPro: IPR002047; AKH.  
 DR PROSITE: PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Flight.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 26.2%; Score 11; DB 1; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1e+05;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 YSP 8  
 DB 4 FTP 6

RESULT 13  
 AKH\_TABAT STANDARD; PRT; 8 AA.  
 AC P14595;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE ADIPOKINETIC HORMONE (AKH) (DIPTERAN CORPORA CARDIACA FACTOR I)  
 DE (DCC I).

OS Tabanus atratus (Horse fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Tabanomorpha;  
 OC Tabanidae; Tabanus.  
 OX NCBI\_TaxID=7207;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE-Corpora cardiaca;  
 RX MEDLINE=90046758; PubMed=2813385;  
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,  
 RA Vogel V.W., Zhang Y.-S., Hayes D.K.;  
 RT "Primary structure of two neurotrophic hormones with adipokinetic and  
 RT hypothalamic activity isolated from the corpora cardiaca of horse  
 RT flies (Diptera).";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).  
 CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA  
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF  
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT  
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.  
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
 CC PIR: A33995; A33995;  
 DR InterPro: IPR002047; AKH.  
 DR PROSITE: PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Flight.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 26.2%; Score 11; DB 1; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1e+05;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 YSP 8  
 DB 4 FTP 6

RESULT 14  
 ALI5\_CARMA STANDARD; PRT; 8 AA.  
 ID ALI5\_CARMA  
 AC P81818;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE CARCINUSSTATIN 15.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE-Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas.";  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 811 MW; 922879D5AB47687D CRC64;

Query Match 26.2%; Score 11; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1e+05; 0; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0;

QY 6 YS 7  
 II

Db 4 YS 5

RESULT 15  
 AL16 CARMA STANDARD; PRT: 8 AA.  
 AC 81819.  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE CARCINUSTATIN 16.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas.";  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD\_RES 8  
 FT AMIDATION.  
 SQ SEQUENCE 8 AA; 813 MW; 7C286B45AB476878 CRC64;

Query Match 26.2%; Score 11; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred No. 1e+05; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0;

QY 6 YS 7

Db 4 YS 5

Search completed: December 13, 2001, 12:01:34  
 Job time: 297 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 13, 2001, 11:55:37 ; Search time 36.87 Seconds  
(without alignments)  
16.072 Million cell updates/sec

Title: US-09-424-080A-1

Perfect score: 42

Sequence: 1<sub>16</sub>TEKKYSP 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 7407320 residues

Total number of hits satisfying chosen parameters: 15187

Minimum-DB seq length: 8

Maximum-DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_1101.\*  
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2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
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5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
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20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	24	57.1	8	AAW21215	Farnesyl synthetase
2	24	57.1	8	AAW21216	Farnesyl synthetase
3	21	50.0	8	AAW36175	Hepatitis C virus
4	21	50.0	8	AAW08147	Clotting factor VI
5	21	50.0	8	AAW08148	Clotting factor VI
6	21	50.0	8	AAW08149	Clotting factor VI
7	21	50.0	8	AAW08150	Clotting factor VI
8	20	47.6	8	AAW79692	pp60(c-src) kinase
9	20	47.6	8	AAW39531	41y-1 pol peptide
10	20	47.6	8	AAW19720	SEQ ID NO 438 from
11	20	47.6	8	AAW57993	Mouse polyoma midd

12	19	45.2	8	15	AAW72419	Recombinant timoth
13	19	45.2	8	16	AAW79693	pp60(c-src) kinase
14	19	45.2	8	17	AAW05444	SH2-binding peptid
15	19	45.2	8	20	AAW47205	Immunogenic peptid
16	19	45.2	8	20	AAW24894	Peptide vlf 88-95
17	19	45.2	8	20	AAW10292	T cell epitope/MHC
18	19	45.2	8	20	AAW94115	VIF-derived HIV pr
19	19	45.2	8	21	AAW33495	Mouse immunoglobul
20	19	45.2	8	21	AAW57994	Hamster polyoma m
21	18	42.9	8	13	AAW27014	Peptide used in an
22	18	42.9	8	14	AAW27016	Peptide used in an
23	18	42.9	8	14	AAW36250	Hepatitis C virus
24	18	42.9	8	14	AAW36251	Hepatitis C virus
25	18	42.9	8	14	AAW36252	Hepatitis C virus
26	18	42.9	8	14	AAW36253	Hepatitis C virus
27	18	42.9	8	15	AAW42770	Consensus peptide,
28	18	42.9	8	15	AAW57377	Protein-kinase inh
29	18	42.9	8	15	AAW57378	Phosphorylase-kin
30	18	42.9	8	16	AAW79474	HIV gag p17 nuclea
31	18	42.9	8	16	AAW70582	HIV(B35)-1, human
32	18	42.9	8	16	AAW73574	Human TSH receptor
33	18	42.9	8	16	AAW73573	Human TSH receptor
34	18	42.9	8	17	AAW98080	Peptide for use in
35	18	42.9	8	17	AAW98058	Peptide for use in
36	18	42.9	8	17	AAW98060	Peptide for use in
37	18	42.9	8	17	AAW88101	Bovine p32 11-clis-
38	18	42.9	8	17	AAW88189	PECAM-1 gene exon
39	18	42.9	8	18	AAW18339	Bovine p32 11-clis-
40	18	42.9	8	19	AAW64278	mMCP-7 peptide sub
41	18	42.9	8	19	AAW79168	Conserved sequence
42	18	42.9	8	19	AAW53299	CS4-CFA/I family s
43	18	42.9	8	19	AAW53300	CS4-CFA/I family s
44	18	42.9	8	20	AAW39614	CTLA-4 VLD CDRI re
45	18	42.9	8	22	AAW46258	HPV type 16 cyto

## ALIGNMENTS

RESULT 1  
AAW21215  
ID AAW21215 standard; peptide: 8 AA.  
AC AAW21215;  
DT 29-JUL-1997 (first entry)  
DE Farnesyl synthetase derived signal oligopeptide #15.  
XX Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;  
KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;  
KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;  
KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;  
KW gonadolibin precursor; plasminogen activator inhibitor 2; prorenin;  
KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;  
KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;  
KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;  
KW treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;  
KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;  
KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.  
XX Homo sapiens.  
XX OS  
XX W09519568-AL.  
XX PN  
XX W09519568-AL.  
XX PD  
XX 20-JUL-1995.  
XX PF  
XX 12-JAN-1995; 95WO-US00575.  
XX PR  
XX 14-JAN-1994; 94US-0182248.  
XX (RATH/) RATH M.  
XX PA  
XX

PI Rath M;  
 DR WPI; 1995-263953/34.  
 XX  
 XX Identifying signal oligopeptide(s) in protein sequence(s) - shown as  
 PT regions of max. hydrophilicity, used in modulating communication.  
 PT between protein(s)  
 XX  
 XX Claim 5; Page 25; 88pp; English.  
 PS  
 CC The sequences given in AAW21201-560 represent hydrophilic signal oligo-  
 CC peptides. These signal oligopeptides are localised on the surface  
 CC of the protein and are represented by the hydrophilicity maxima of  
 CC the protein. These peptides are enriched in charged amino acids  
 CC arranged with neutral spacer amino acids. The specific signal  
 CC character of these oligopeptides is determined by a characteristic  
 CC combination of conformation and charge within the signal sequence.  
 CC These oligopeptides may be used as vaccines in the treatment of  
 CC human disease, as competitive inhibitors to prevent or reduce the  
 CC metabolic action or interaction of a selected protein by blocking  
 CC its specific signal sequences, or as therapeutic agents to function  
 CC as feedback regulators to reduce synthesis rate of a selected protein.  
 CC These peptides may be modified by omitting one or more amino acids at  
 CC the N- and/or C-terminal, by substituting one or more amino acids  
 CC without consideration of charge and polarity, by substituting one or  
 CC more amino acids with amino acid residues with similar charge and/or  
 CC polarity, by omitting one or more amino acids or a combination of these.  
 XX  
 XX Sequence 8 AA;  
 SQ

Query Match 57.1%; Score 24; DB 16; Length 8;  
 Best Local Similarity 80.0%; Pred. No. 4.3e+05;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 TEKRY 6  
 DB 3 tekry 7  
 III:I

RESULT 2  
 AAW21216  
 ID AAW21216 standard; peptide; 8 AA.  
 XX  
 AC AAW21216;  
 XX  
 DT 29-JUL-1997 (first entry)  
 XX  
 DE Farnesyl synthetase derived signal oligopeptide #16.  
 XX  
 KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; HIV;  
 KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;  
 KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;  
 KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;  
 KW gonadoliben precursor; plasminogen activator inhibitor 2; proteinin;  
 KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;  
 KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVWS;  
 KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;  
 KW treponema pallidum membrane protein; TMPA; Islet amyloid polypeptide;  
 KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;  
 KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.  
 XX  
 OS Homo sapiens.  
 XX  
 XX W09519568-A1.  
 PN  
 XX 20-JUL-1995.  
 PD  
 XX 12-JAN-1995; 95WO-US00575.  
 PP  
 XX 14-JAN-1994; 94US-0182249.  
 PR  
 XX (RATH,/) RATH M.  
 PA

XX Rath M;  
 PI WPI; 1995-263953/34.  
 DR  
 XX Identifying signal oligopeptide(s) in protein sequence(s) - shown as  
 PT regions of max. hydrophilicity, used in modulating communication  
 PT between protein(s)  
 XX  
 XX Claim 5; Page 25; 88pp; English.  
 PS  
 CC The sequences given in AAW21201-560 represent hydrophilic signal oligo-  
 CC peptides. These signal oligopeptides are localised on the surface  
 CC of the protein and are represented by the hydrophilicity maxima of  
 CC the protein. These peptides are enriched in charged amino acids  
 CC arranged with neutral spacer amino acids. The specific signal  
 CC character of these oligopeptides is determined by a characteristic  
 CC combination of conformation and charge within the signal sequence.  
 CC These oligopeptides may be used as vaccines in the treatment of  
 CC human disease, as competitive inhibitors to prevent or reduce the  
 CC metabolic action or interaction of a selected protein by blocking  
 CC its specific signal sequences, or as therapeutic agents to function  
 CC as feedback regulators to reduce synthesis rate of a selected protein.  
 CC These peptides may be modified by omitting one or more amino acids at  
 CC the N- and/or C-terminal, by substituting one or more amino acids  
 CC without consideration of charge and polarity, by substituting one or  
 CC more amino acids with amino acid residues with similar charge and/or  
 CC polarity, by omitting one or more amino acids or a combination of these.  
 XX  
 XX Sequence 8 AA;  
 SQ

Query Match 57.1%; Score 24; DB 16; Length 8;  
 Best Local Similarity 80.0%; Pred. No. 4.3e+05;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 TEKRY 6  
 DB 3 tekry 7  
 III:I

RESULT 3  
 AAR36175  
 ID AAR36175 standard; peptide; 8 AA.  
 XX  
 AC AAR36175;  
 XX  
 DT 24-MAY-1993 (first entry)  
 XX  
 DE Hepatitis C virus (HCV) epitope EpEE.  
 XX  
 KW Hepatitis; liver disease; HCV1; monoclonal antibody; epitope;  
 KW immobilised reagent; immunoassay; diagnosis; detection; treatment;  
 KW infection.  
 XX  
 OS Hepatitis C virus type 1.  
 XX  
 PN W09300365-A.  
 PD 07-JAN-1993.  
 XX  
 XX 24-JUN-1992; 92WO-US05388.  
 PF  
 XX 24-JUN-1991; 91US-0722489.  
 PR  
 XX (CHIR ) CHIRON CORP.  
 PA  
 XX Chien DY, Rutter W;  
 PI WPI; 1993-036334/04.  
 DR  
 XX Polypeptide(s) comprising truncated hepatitis C virus sequences -  
 PT for detection, prevention and treatment of hepatitis C infection  
 PT

XX Example A; Page 39; 80pp; English.

XX This octamer was found to be immunoreactive with anti-HCV anti-sera.  
 CC In the epitope mapping experiment three different samples of anti-sera  
 CC were reacted with the peptide octamer and then incubated with  
 CC HRP-labelled goat anti-human IgG antiserum to enable detection of  
 CC binding. This epitope starts from amino acid 2676 of the HCV  
 CC polyprotein.  
 CC This was found to be a particularly strong epitope.

XX Sequence 8 AA;

Query Match 50.0%; Score 21; DB 14; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 4.3e+05;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERKY 6  
 DB 1 iterly 6

RESULT 4  
 AAY08147  
 ID AAY08147 standard; peptide; 8 AA.

XX AC AAY08147;  
 XX DT 09-JUL-1999 (first entry)

XX Clotting factor VIII binding peptide 29.

XX Coagulation factor VIII; clotting factor VIII; diagnosis; treatment;  
 KW purification; disorder; blood coagulation.

XX OS Synthetic.

XX PN W09914232-AL.

XX PD 25-MAR-1999.

XX PF 12-SEP-1998; 98WO-EP05822.

XX PR 13-SEP-1997; 97DE-1040310.

XX PA (OCTA-) OCTAPHARMA AG.

XX PI Jungbauer A;

XX DR WPI; 1999-312410/26.

XX Peptides with affinity for blood clotting factor 8

PS Claim 4; Page 26; 51pp; German.

XX This invention describes novel peptides (AAY08119-Y08212) with affinity  
 CC for coagulation factor VIII which can be used for labeling,  
 CC identification (diagnostic) and purification of factor VIII. Some are  
 CC specific for one of natural and recombinant factor VIII, others are  
 CC reactive with both forms. Factor VIII is used to treat disorders of  
 CC blood coagulation. Using relatively small peptides, rather than large  
 CC antibody molecules generally used, simplifies purification of factor  
 CC VIII. The peptides are of formula R1-X-R2 where R1 = amino or a  
 CC peptide; R2 = carboxy or a peptide and X = a peptide of at least 3,  
 CC preferably 7-12, amino acid residues.

XX Sequence 8 AA;

Query Match 50.0%; Score 21; DB 20; Length 8;  
 Best Local Similarity 60.0%; Pred. No. 4.3e+05;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKYSF 8  
 DB 4 keyap 8

RESULT 5

AAY08148  
 ID AAY08148 standard; peptide; 8 AA.

XX AC AAY08148;

XX DT 09-JUL-1999 (first entry)

XX Clotting factor VIII binding peptide 30.

XX Coagulation factor VIII; clotting factor VIII; diagnosis; treatment;  
 KW purification; disorder; blood coagulation.

XX OS Synthetic.

XX PN W09914232-AL.

XX PD 25-MAR-1999.

XX PF 12-SEP-1998; 98WO-EP05822.

XX PR 13-SEP-1997; 97DE-1040310.

XX PA (OCTA-) OCTAPHARMA AG.

XX PI Jungbauer A;

XX DR WPI; 1999-312410/26.

XX Peptides with affinity for blood clotting factor 8

PS Claim 4; Page 26; 51pp; German.

XX This invention describes novel peptides (AAY08119-Y08212) with affinity  
 CC for coagulation factor VIII which can be used for labeling,  
 CC identification (diagnostic) and purification of factor VIII. Some are  
 CC specific for one of natural and recombinant factor VIII, others are  
 CC reactive with both forms. Factor VIII is used to treat disorders of  
 CC blood coagulation. Using relatively small peptides, rather than large  
 CC antibody molecules generally used, simplifies purification of factor  
 CC VIII. The peptides are of formula R1-X-R2 where R1 = amino or a  
 CC peptide; R2 = carboxy or a peptide and X = a peptide of at least 3,  
 CC preferably 7-12, amino acid residues.

XX Sequence 8 AA;

Query Match 50.0%; Score 21; DB 20; Length 8;  
 Best Local Similarity 60.0%; Pred. No. 4.3e+05;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKYSF 8  
 DB 3 keyap 7

RESULT 6

AAY08149  
 ID AAY08149 standard; peptide; 8 AA.

XX AC AAY08149;

XX DT 09-JUL-1999 (first entry)

XX Clotting factor VIII binding peptide 31.

XX Coagulation factor VIII; clotting factor VIII; diagnosis; treatment;



KW purification; disorder; blood coagulation.

OS Synthetic.

PN WO9914232-A1.

XX 25-MAR-1999.

PD 12-SEP-1998; 98WO-EP05822.

PR 13-SEP-1997; 97DE-1040310.

XX (OCTA-) OCTAPHARMA AG.

PI Jungbauer A;

XX WPI; 1999-312410/26.

PT Peptides with affinity for blood clotting factor 8

PS Claim 4; Page 27; 51pp; German.

XX This invention describes novel peptides (AAY08119-Y08212) with affinity for coagulation factor VIII which can be used for labeling, identification (diagnostic) and purification of factor VIII. Some are specific for one of natural and recombinant factor VIII, others are reactive with both forms. Factor VIII is used to treat disorders of blood coagulation. Using relatively small peptides, rather than large antibody molecules generally used, simplifies purification of factor VIII. The peptides are of formula R1-X-R2 where R1 = amino or a peptide; R2 = carboxy or a peptide and X = a peptide of at least 3, preferably 7-12, amino acid residues.

XX Sequence 8 AA;

Query Match 50.0%; Score 21; DB 20; Length 8;

Best Local Similarity 60.0%; Pred. No. 4.3e+05;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKYSP 8

DB 2 keyap 6

RESULT 7

AAV08150  
ID AAY08150 standard; peptide; 8 AA.

AC AAY08150;

DT 09-JUL-1999 (first entry)

DE Clotting factor VIII binding peptide 32.

XX Coagulation factor VIII; clotting factor VIII; diagnosis; treatment; purification; disorder; blood coagulation.

OS Synthetic.

PN WO9914232-A1.

XX 25-MAR-1999.

PD 12-SEP-1998; 98WO-EP05822.

PR 13-SEP-1997; 97DE-1040310.

XX (OCTA-) OCTAPHARMA AG.

PI Jungbauer A;

XX WPI; 1999-312410/26.

XX Peptides with affinity for blood clotting factor 8

XX Claim 4; Page 27; 51pp; German.

XX This invention describes novel peptides (AAY08119-Y08212) with affinity for coagulation factor VIII which can be used for labeling, identification (diagnostic) and purification of factor VIII. Some are specific for one of natural and recombinant factor VIII, others are reactive with both forms. Factor VIII is used to treat disorders of blood coagulation. Using relatively small peptides, rather than large antibody molecules generally used, simplifies purification of factor VIII. The peptides are of formula R1-X-R2 where R1 = amino or a peptide; R2 = carboxy or a peptide and X = a peptide of at least 3, preferably 7-12, amino acid residues.

XX Sequence 8 AA;

XX Query Match 50.0%; Score 21; DB 20; Length 8;

XX Best Local Similarity 60.0%; Pred. No. 4.3e+05;

XX Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKYSP 8

DB 1 keyap 5

RESULT 8

AAV79692

ID AAR79692 standard; peptide; 8 AA.

AC AAR79692;

XX 27-FEB-1996 (first entry)

DE pp60(c-src) kinase phosphorylation site in mouse polyoma middle t Ag.

XX Peptide library; phosphorylation site; protein kinase; substrate; inhibitor; competitor; cellular response; cell cycle control;

KW Immune response; transcriptional activation; cell development.

OS Synthetic.

PN WO9518823-A2.

XX 13-JUL-1995.

PD 06-JAN-1995; 95WO-US00147.

PR 07-JAN-1994; 94US-0178570.

XX (BETH-) BETH ISRAEL HOSPITAL ASSOC.

PI Cantley LC, Songyang Z;

XX WPI; 1995-255036/33.

XX Determ. of amino acid sequence of protein kinase phosphorylation

PT site - by phosphorylation of peptide library and sequencing

PT phospho-peptide(s) formed, also new substrates and their analogues

PT for modulating or detecting protein kinase

XX Example 7; Page 36; 131pp; English.

XX An oriented degenerate peptide library of the amino acid formula

CC AAR79692 was constructed to isolate the amino acid sequences at the

CC phosphorylation sites of a protein kinase eg. protein kinase A,

CC cyclin B/p33(cdc2), src family kinases, etc. Peptides which are

CC phosphorylated are isolated and their amino acid sequences are compared

CC to known substrate/inhibitor peptide sequences for that protein kinase.

CC The peptides AAR79692-R79700 represent phosphorylation sites for the src

CC family kinases pp60(c-src) or pp60(v-src). This peptide sequence is the

CC phosphorylation site in the mouse polyoma middle t antigen at Tyr315.  
 CC The isolated peptides can be used to screen cpds. for effects on the  
 CC protein kinase activity, generate antibodies to identify native kinase  
 CC substrates, or modulate a variety of cellular responses in which protein  
 CC kinases are involved eg. cell cycle control, immune response,  
 CC transcriptional activation or cell development.  
 XX  
 SQ Sequence 8 AA;

Query Match 47.6%; Score 20; DB 16; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 4.3e+05;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 EKKYSP 8  
 Db 1 eeymp 6

RESULT 9

AAW39531  
 ID AAW39531 standard; peptide; 8 AA.

XX AAW39531;

AC AAW39531;

DT 11-JUN-1998 (first entry)

XX HIV-1 pol peptide (pos. 184-191) capable of binding to HLA-A\*0301.

XX T cell epitope; immune response; human leukocyte antigen; HLA Class I;  
 KW vaccine; immunogenic; major histocompatibility complex; MHC; B cell;  
 KW disease; anti-tumour; anti-viral.

XX Human immunodeficiency virus type 1.

OS WO9741440-A1.

XX 06-NOV-1997.

PD 28-APR-1997; 97WO-NL00229.

XX 23-DEC-1996; 96EP-0203670.

PR 26-APR-1996; 96EP-0201145.

XX (UYLE-) RIJKSUNIV LEIDEN.

XX (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.

XX Kast WM, Melief CJM, Offringa R, Toes REM, Van Der Burg SH;

XX WPI; 1997-549891/50.

XX Method of selecting T cell peptide epitope(s) - by measuring the  
 PT stability of HLA class I-peptide complexes on intact B cells.

XX Example 2; Page 62; 109pp; English.

XX Peptides AAW39430-W39734 are used in a novel method for the selection of  
 CC immunogenic T-cell peptide epitopes present in polypeptide antigens. The  
 CC method involves the identification of peptide sequences capable of  
 CC binding to an HLA (human leukocyte antigen) class I molecule and  
 CC measuring the binding of this epitope peptide to the HLA class I  
 CC peptide. The stability of binding of the peptide and MHC (major  
 CC histocompatibility complex) class I molecule is measured on intact human  
 CC B cells carrying the MHC molecule at their cell surfaces. The method can  
 CC be used to select peptide epitopes for generating vaccines against a  
 CC disease associated with the polypeptide, e.g. cancers or AIDS. The  
 CC peptide epitopes are especially T-cell peptide epitopes with strong  
 CC anti-tumour and anti-viral immune responses. Peptides AAW39528-W39547 are  
 CC conserved human immunodeficiency virus type 1 (HIV-1) pol sequences which  
 CC are compliant with the HLA-A\*0301 binding motif.

XX Sequence 8 AA;

Query Match 47.6%; Score 20; DB 18; Length 8;  
 Best Local Similarity 80.0%; Pred. No. 4.3e+05;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTEKK 5  
 Db 2 lteek 6

RESULT 10

AAAY19720  
 ID AAY19720 standard; Protein; 8 AA.

XX AAY19720;

AC AAY19720;

DT 14-JUL-1999 (first entry)

XX SEQ ID NO 438 from WO9922243.

XX Human secreted protein; cancer; tumour; neurodegenerative disorder;  
 KW developmental abnormality; fetal deficiency; blood disorder; leukemia;  
 KW immune system disease; autoimmune disease; hepatic disease;  
 KW renal disease; lymphoma; inflammation; allergy; ischemic shock;  
 KW Alzheimer's; cognitive disorder; schizophrenia; prostate disease;  
 KW obesity; osteoclast; osteoporosis; arthritis; malignancy; testes disease;  
 KW lung disease; thymus disease; digestive disorder; endocrine disorder;  
 KW infection; AIDS.

XX Homo sapiens.

OS WO9922243-A1.

XX 06-MAY-1999.

PD 23-OCT-1998; 98WO-US22376.

XX 24-OCT-1997; 97US-0063387.

XX 24-OCT-1997; 97US-0062784.

XX 24-OCT-1997; 97US-0063088.

XX 24-OCT-1997; 97US-0063089.

XX 24-OCT-1997; 97US-0063090.

XX 24-OCT-1997; 97US-0063091.

XX 24-OCT-1997; 97US-0063092.

XX 24-OCT-1997; 97US-0063097.

XX 24-OCT-1997; 97US-0063098.

XX 24-OCT-1997; 97US-0063099.

XX 24-OCT-1997; 97US-0063100.

XX 24-OCT-1997; 97US-0063101.

XX 24-OCT-1997; 97US-0063109.

XX 24-OCT-1997; 97US-0063110.

XX 24-OCT-1997; 97US-0063111.

XX 24-OCT-1997; 97US-0063148.

XX 24-OCT-1997; 97US-0063386.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Brewer LA, Carter KC, Duan DR, Ebner R, Endress GA;  
 XX Feng P, Florence C, Florence KA, Greene JM, Janat F;  
 XX Kaye H, Lafleur DW, Moore PA, Ni J, Olsen HS, Rosen CH;  
 XX Ruben SM, Shi Y, Soppet DR, Wei Y, Young P;

XX WPI; 1999-303069/25.

XX New isolated human genes and the secreted polypeptides they encode

XX Disclosure; Page 508; 546pp; English.

XX The specification describes human secreted proteins. The polynucleotides  
 CC and their corresponding secreted polypeptides are useful for preventing,  
 CC treating or ameliorating medical conditions, e.g. by protein or gene  
 CC therapy. Pathological conditions can also be diagnosed by determining  
 CC the amount of the polypeptides in a sample or by determining the presence

CC of mutations in the polynucleotides. Specific uses are described for each  
 CC of the polynucleotides, based on which tissues they are most highly  
 CC expressed in, and include developing products for the diagnosis or  
 CC treatment of cancer, tumours, neurodegenerative disorders, developmental  
 CC abnormalities and fetal deficiencies, blood disorders, leukemias,  
 CC diseases of the immune system, autoimmune diseases, hepatic and renal  
 CC diseases, lymphomas, inflammation, allergies, ischemic shock, Alzheimer's  
 CC and cognitive disorders, osteoclasts such as osteoporosis, arthritis or  
 CC malignancies, diseases of testes, lung or thymus, digestive/endocrine  
 CC disorders, infections and AIDS. The polypeptides are also useful for  
 CC identifying their binding partners.

XX Sequence 8 AA;

Query Match 47.6%; Score 20; DB 20; Length 8;  
 Best Local Similarity 80.0%; Pred. No. 4.3e+05;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERK 5  
 DB 3 lsekk 7

RESULT 11

AAV57993  
 ID AAV57993 standard; peptide; 8 AA.

XX AAV57993;

XX 23-MAR-2000 (first entry)

XX Mouse polyoma middle t (Y315) peptide SEQ ID NO:47.

XX Protein kinase; phosphorylation site; signal transduction.

XX Mus sp.

XX US6004757-A.

XX 21-DEC-1999.

XX 06-JAN-1995; 95US-0369643.

XX 07-JAN-1994; 94US-0178570.

XX (BETH-) BETH ISRAEL HOSPITAL ASSOC.

XX Cantley LC, Songyang Z;

XX WPI; 2000-096301/08.

XX Peptide substrate for a kinase, useful for determining substrate  
 PT specificity -

XX Example 7; Column 34; 69pp; English.

XX The present invention describes a substrate for lck comprising a 9 amino  
 CC acid peptide (I). Also described is a method of inhibiting kinase  
 CC activity of lck by contacting it with (I) in vitro. The peptide is  
 CC useful for determining substrate specificity of a protein kinase.  
 CC Information on the substrate specificity of protein kinases in signal  
 CC transduction would provide an insight into signal transduction  
 CC mechanisms and could allow for the design of therapeutic agents. The  
 CC present sequence represents a peptide used in the exemplification of  
 CC the present invention.

XX Sequence 8 AA;

Query Match 47.6%; Score 20; DB 21; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 4.3e+05;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 EKKYSP 8  
 DB 1 eekymp 6

RESULT 12

AAV72419  
 ID AAV72419 standard; Peptide; 8 AA.

XX AAV72419;

XX 21-JUN-1995 (first entry)

XX Recombinant timothy grass allergen Phl pII epitope AS 69-76.

XX Timothy grass; Phleum pratense; allergen; recombinant; group II/III;  
 KW grass; plant; pollen; B-cell; T-cell; epitope; detection; allergy.

XX Phleum pratense.

XX WO9423035-A.

XX 13-OCT-1994.

XX 31-MAR-1994; 94WO-AT000039.

XX 01-APR-1993; 93AT-0000672.

XX (BIOM-) BIOMAY PRODN & HANDELSGES MBH.

XX Dollecek C, Kraft D, Laffer S, Scheiner O, Steinberger P;  
 PI Valenta R, Vrtala S;

XX WPI; 1994-333195/41.

XX Recombinant timothy grass pollen allergen Phl p II - useful in a  
 PT process for the in-vitro detection of Phl p II allergies and for  
 PT the treatment of pollen allergies in mammals

XX Disclosure; Fig 3; 24pp; German.

XX A series of synthetic B-cell epitopes (AAV72414-20) generated from the  
 CC amino acid sequence (AAR63207) of the timothy grass allergen Phl pII.  
 CC The gene (AAQ77731) encodes a protein of 122 a.a. including a 26 a.a.  
 CC signal peptide sequence. This is the first complete recombinant allergen  
 CC from the group II/III plant pollen allergens. The allergen or its  
 CC epitopes can be used in the detection of either an allergy in a patient  
 CC against the Phl pII allergen or a cellular reaction to the allergen.  
 CC Mammalian pollen allergy may be treated using recombinant or synthetic  
 CC Phl pII or at least one of its epitopes.

XX Sequence 8 AA;

Query Match 45.2%; Score 19; DB 15; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTERK 4  
 DB 1 lterk 4

RESULT 13

AAV79693  
 ID AAV79693 standard; peptide; 8 AA.

XX AAV79693;

XX 27-FEB-1996 (first entry)

DE pp60(c-src) kinase phosphorylation site in hamster polyoma middle t Ag.  
 XX Peptide library; phosphorylation site; protein kinase; substrate;  
 KW inhibitor; competitor; cellular response; cell cycle control;  
 KW immune response; transcriptional activation; cell development.  
 XX Synthetic.  
 XX W09518823-A2.  
 XX 13-JUL-1995.  
 XX 06-JAN-1995; 95WO-US00147.  
 XX 07-JAN-1994; 94US-0178570.  
 XX (BETH-) BETH ISRAEL HOSPITAL ASSOC.  
 XX Cantley LC, Songyang Z;  
 XX WPI; 1995-255036/33.  
 XX Determn. of amino acid sequence of protein kinase phosphorylation  
 XX site - by phosphorylation of peptide library and sequencing.  
 XX phospho-peptides formed, also new substrates and their analogues  
 XX for modulating or detecting protein kinase  
 XX Example 7; Page 36; 131pp; English.  
 XX An oriented degenerate peptide library of the amino acid formula  
 XX AAR9661 was constructed to isolate the amino acid sequences at the  
 XX phosphorylation sites of a protein kinase eg. protein kinase A,  
 XX cyclin B/p33(cdc2), src family kinases, etc. Peptides which are  
 XX phosphorylated are isolated and their amino acid sequences are compared.  
 XX To known substrate/inhibitor peptide sequences for that protein kinase.  
 XX The peptides AAR79689-R79700 represent phosphorylation sites for the src  
 XX family kinases pp60(c-src) or pp60(v-src). This peptide sequence is the  
 XX phosphorylation site in hamster polyoma middle t antigen at Tyr295.  
 XX The isolated peptides can be used to screen opds. for effects on the  
 XX protein kinase activity, generate antibodies to identify native kinase  
 XX substrates, or modulate a variety of cellular responses in which protein  
 XX kinases are involved eg. cell cycle control, immune response,  
 XX transcriptional activation or cell development.  
 XX Sequence 8 AA;

Query Match 45.2%; Score 19; DB 16; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 4.3e+05;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 EKQYSP 8  
 Db 1 eneymp 6

RESULT 14  
 AAR05444  
 ID AAR05444 standard; Peptide; 8 AA.  
 XX  
 AC AAR05444;  
 XX  
 DT 24-FEB-1998 (first entry)  
 DE SH2-binding peptide for Grb2.

XX Src-homology region 3 domain; human; mouse; SH3 domain; cell growth;  
 KW cellular signalling element; cellular structural element; malignancy;  
 KW protein identification; functional domain; protein screening;  
 KW cellular signal transduction process; binding peptide.  
 XX Synthetic.  
 OS  
 OS Homo sapiens.

PN W09631625-A1.  
 XX 10-OCT-1996.  
 XX 04-APR-1996; 96WO-US04454.  
 XX 03-APR-1996; 96US-0630915.  
 XX 07-APR-1995; 95US-0417872.  
 XX (CYTO-) CYTOGEN CORP.  
 XX (UYNC-) UNIV NORTH CAROLINA.  
 XX Fowlkes DM, Hoffman N, Kay BK, McConnell SJ, Sparks AB;  
 XX WPI; 1996-465045/46.  
 XX Identifying polypeptide(s) having specific functional domain (esp.  
 XX SH3 domain) - comprises detecting selective binding to recognition  
 XX unit, regardless of sequence homology  
 XX Example; Page 92; 174pp; English.  
 XX AAR05438-W05444 represent Src-homology region 2 (SH2) domain binding  
 XX peptides. These sequences were used as parts of multivalent recognition  
 XX unit complexes used in the method of the invention. The method of the  
 XX invention is for identifying polypeptides containing functional domains  
 XX of interest, especially Src-homology region 3 (SH3) domains. It  
 XX comprises contacting a multivalent recognition unit (RU) complex with a  
 XX number of peptides and identifying polypeptides having a selective  
 XX binding affinity for the RU complex. The method is based on functional  
 XX similarities and does not rely on sequence similarities. Prior methods  
 XX only gave limited success for identifying proteins containing an SH3  
 XX domain due to the minimal sequence homology among known SH3 proteins.  
 XX Multivalent RU complexes are particularly suited to screening for  
 XX polypeptides containing functional domains that are similar to, but not  
 XX identical in sequence to, the original target functional domain. The new  
 XX method enables proteins having a common function to be identified.  
 XX Identification of novel SH3 proteins will be useful for a better  
 XX understanding of cell growth, malignancy, signal transduction processes,  
 XX etc. New candidate drugs can be identified, and their specificities  
 XX (e.g. pharmacological activities) can be assessed using the method of  
 XX the invention.  
 XX Sequence 8 AA;

Query Match 45.2%; Score 19; DB 17; Length 8;  
 Best Local Similarity 60.0%; Pred. No. 4.3e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 KQYSP 8  
 Db 4 qnysp 8

RESULT 15  
 AAY47205  
 ID AAY47205 standard; Peptide; 8 AA.  
 XX  
 AC AAY47205;  
 XX  
 DT 01-DEC-1999 (first entry)  
 DE Immunogenic peptide having a human leukocyte antigen binding motif #1816.  
 XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;  
 KW immune response; T cell activation; major histocompatibility complex;  
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;  
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;  
 KW vaccine; immunisation.  
 XX Synthetic.  
 OS  
 OS Homo sapiens.

XX WO9945954-A1.  
 XX PN  
 XX 16-SEP-1999.  
 XX PD  
 XX PF  
 XX 13-MAR-1998; 98WO-US05039.  
 XX PR  
 XX 13-MAR-1998; 98WO-US05039.  
 XX PA  
 XX (EPIM-) EPIMUNE INC.  
 PI Sette A, Kubo RT, Sidney J, Cells E, Grey HM, Southwood S;  
 XX WPI; 1999-551214/46.  
 XX  
 XX New immunogenic peptides with HLA binding motif, useful in treatment  
 XX and diagnosis of cancers and viral diseases  
 XX  
 XX Claim 1; Page 98; 150pp; English.  
 XX  
 CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides  
 CC having a human major histocompatibility complex (MHC) Class I (also  
 CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic  
 CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes  
 CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell  
 CC response against the antigen from which the peptide is derived.  
 CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are  
 CC normally induced by an antigen in the form of a peptide fragment bound  
 CC to a HLA molecule, rather than the intact foreign antigen itself, and  
 CC are particularly important in tumour rejection and in fighting viral  
 CC infections. The peptides are therefore useful therapeutically to treat  
 CC or prevent viral infections and cancers in mammals (especially humans)  
 CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.  
 CC They can be administered as vaccines to elicit an immune response in  
 CC individuals susceptible or otherwise at risk of viral infection or  
 CC cancer, or used to treat chronic or acute conditions. They are also  
 CC useful diagnostically, and can be used to induce a cytotoxic T cell  
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to  
 CC produce CTLs ex vivo for infusion back into a patient. The  
 CC polynucleotides encoding the immunogenic peptides are also useful  
 CC therapeutically and for immunisation as above.  
 XX  
 XX Sequence 8 AA;

Query Match 45.28; Score 19; DB 20; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 4.3e+05;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LTKKY 6  
 | : : :  
 Db 2 lvqky 7

Search completed: December 13, 2001, 11:57:18  
 Job time: 101 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 13, 2001, 11:56:34 ; Search time 22.27 Seconds

(without alignments)  
27.364 Million cell updates/sec

Title: US-09-424-080A-2

Perfect score: 11

Sequence: 1: LXXXXXX 8

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 147

Minimum DB seq length: 8

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.68.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	8	1 LFSAME	probable msra leader
2	4	36.4	8	2 A32523	peptidyl-di-peptida
3	4	36.4	8	2 A61348	red pigment-concen
4	4	36.4	8	2 S08996	hypertrehalosemic
5	4	36.4	8	2 B49823	adipoknetic hormo
6	4	36.4	8	2 B44960	neurokinetic Led-C
7	4	36.4	8	2 S15422	adipoknetic hormo
8	4	36.4	8	2 A43976	hypertrehalosemic
9	4	36.4	8	2 B43976	adipoknetic hormo
10	4	36.4	8	2 A33995	adipoknetic hormo
11	4	36.4	8	2 S11345	adipoknetic hormo
12	4	36.4	8	2 A58641	ig heavy chain v r
13	4	36.4	8	2 P81407	sperm-activating p
14	4	36.4	8	2 E60588	sperm-activating p
15	4	36.4	8	2 F60588	sperm-activating p
16	4	36.4	8	2 G60588	neuropeptide B - b
17	4	36.4	8	2 B24749	neuropeptide B - b
18	4	36.4	8	2 T10077	hypothetical prote
19	4	36.4	8	2 FC4131	hypothetical prote
20	4	36.4	8	2 FC1002	leucine--trna liga
21	4	36.4	8	2 S65647	2-hydroxyglutaryl-
22	4	36.4	8	2 A39308	glycine reductase
23	4	36.4	8	2 T48890	hypothetical prote
24	4	36.4	8	2 A37521	R-phycocerythrin ga
25	4	36.4	8	2 S68802	nitrate reductase
26	4	36.4	8	2 S16324	hypothetical prote
27	4	36.4	8	2 PA0035	protein QA300039 -
28	4	36.4	8	2 PA0032	protein QA300040 -
29	4	36.4	8	2 T10952	hypothetical prote

30	4	36.4	8	2 T14906	hypothetical prote
31	4	36.4	8	2 G33098	205K exoantigen -
32	4	36.4	8	2 A23967	leucopyrokinin - M
33	4	36.4	8	2 S21663	neuropeptide - flo
34	4	36.4	8	2 S65846	cardioacceleratory
35	4	36.4	8	2 D47393	neuropeptide calla
36	4	36.4	8	2 P70368	ig gamma chain C r
37	4	36.4	8	2 P70398	ig heavy chain CHD
38	4	36.4	8	2 P70311	ig heavy chain CHD
39	4	36.4	8	2 P70323	enamelin f - bovin
40	4	36.4	8	2 S10783	thymic humoral fac
41	4	36.4	8	2 A28719	fibroblast growth
42	4	36.4	8	2 A42057	ig H chain V-D-J r
43	4	36.4	8	2 P81618	phosphatidylethano
44	4	36.4	8	2 P80043	cytochrome oxidase
45	4	36.4	8	2 T13818	

#### ALIGNMENTS

RESULT 1

LFSAME

probable msra leader peptide - Staphylococcus epidermidis

C:Species: Staphylococcus epidermidis

C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999

C:Accession: S11157

R:Ross, J. I.; Eady, E. A.; Cove, J. H.; Cunliffe, W. J.; Baumberg, S.; Wootton, J. C.

Mol. Microbiol. 4, 1207-1214, 1990

A:Title: Inducible erythromycin resistance in staphylococci is encoded by a member of

A:Reference number: S11157; MUID:91041730

A:Accession: S11157

A:Molecule type: DNA

A:Residues: 1-8 <ROS>

C:Cross-references: EMBL:X52085; NID:g47000; PIDN:CAA36303.1; PID:g581653

C:Superfamily: probable msra leader peptide

Query Match 36.4%; Score 4; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1

DB 7 L 7

RESULT 2

A32523

peptidyl-di-peptidase A (EC 3.4.15.1) - bovine (fragment)

N:Alternate names: angiotensin I-converting enzyme; peptidyl-di-peptidase I

C:Species: Bos primigenius taurus (cattle)

C>Date: 18-Oct-1989 #sequence\_revision 18-Oct-1989 #text\_change 11-May-2000

C:Accession: A32523

R:Harris, R. B.

Adv. Exp. Med. Biol. 198, 513-521, 1986

A:Title: Isolation and sequencing of an active-site peptide from angiotensin I-conver

A:Reference number: A32523; MUID:87123961

A:Accession: A32523

A:Molecule type: protein

A:Residues: 1-8 <HAR>

C:Superfamily: mammalian peptidyl-di-peptidase A

C:Keywords: alternative splicing; blood pressure control; peptidyl-di-peptide hydrolase

Query Match 36.4%; Score 4; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1

DB 4 L 4

RESULT 3  
A61348  
red pigment-concentrating hormone - northern shrimp  
N:Alternate names: blanching hormone  
C:Species: Pandalus borealis (northern shrimp)  
C:Date: 02-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 07-May-1999  
C:Accession: A61348; S07139  
R:Fernlund, P.; Josefsson, L.  
Science 177, 173-175, 1972  
A:Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.  
A:Reference number: A61348; MUID:72228738  
A:Accession: A61348  
A:Molecule type: protein  
A:Residues: 1-8 <FER1>  
R:Fernlund, P.  
Biochim. Biophys. Acta 371, 304-311, 1974  
A:Title: Structure of the red-pigment-concentrating hormone of the shrimp, Pandalus borealis  
A:Reference number: S07139; MUID:75054965  
A:Accession: S07139  
A:Molecule type: protein  
A:Residues: 'E', 2-8 <FER2>  
A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
C:Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pi-  
zed pigment-containing cells.  
C:Superfamily: adipokinetic hormone  
C:Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutamic  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:8/Modified site: amidated carboxyl end (trp) #status experimental

Query Match 36.4%; Score 4; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 L 1  
Db 2 L 2  
RESULT 4  
S08996  
hypertrehalosemic hormone II - oriental cockroach  
N:Alternate names: Pea-CAH-II  
C:Species: Blatta orientalis (oriental cockroach)  
C:Date: 30-Jun-1992 #sequence\_revision 24-Oct-1997 #text\_change 31-Oct-1997  
C:Accession: S08996  
R:Gaede, G.; Rinehart, K.L.  
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990  
A:Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora  
entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard  
A:Reference number: S08995; MUID:90253659  
A:Accession: S08996  
A:Molecule type: protein  
A:Residues: 1-8 <GAP>  
A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
C:Superfamily: adipokinetic hormone  
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:8/Modified site: amidated carboxyl end (trp) #status experimental

Query Match 36.4%; Score 4; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 L 1  
Db 2 L 2  
RESULT 5  
B49823  
adipokinetic hormone - cockchafer  
N:Alternate names: Melolontha melolontha (cockchafer)  
C:Species: Melolontha melolontha (cockchafer)  
C:Date: 19-Mar-1997 #sequence\_revision 31-Oct-1997 #text\_change 31-Oct-1997  
C:Accession: S15422  
R:Gaede, G.  
Biochem. J. 275, 671-677, 1991  
A:Title: A unique charged tyrosine-containing member of the adipokinetic hormone/red  
A:Reference number: S15422; MUID:91248100  
A:Accession: S15422

adipokinetic hormone II - American cockroach  
N:Alternate names: neuropeptide M-II; periplanetin CC-1  
C:Species: Periplaneta americana (American cockroach)  
C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 07-May-1999  
C:Accession: B49823; A05170  
R:Scarborough, R.M.; Jamieson, G.C.; Kallish, F.; Kramer, S.J.; McEnroe, G.A.; Miller,  
Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984  
A:Title: Isolation and primary structure of two peptides with cardioacceleratory and  
A:Reference number: A49823; MUID:84298179  
A:Accession: B49823  
A:Molecule type: protein  
A:Residues: 1-8 <SCA>  
R:Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr.,  
Biochem. Biophys. Res. Commun. 124, 350-358, 1984  
A:Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment  
A:Reference number: A90118; MUID:85046530  
A:Accession: A05170  
A:Molecule type: protein  
A:Residues: 'E', 2-8 <WIT>  
C:Superfamily: adipokinetic hormone  
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyrogluta  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:8/Modified site: amidated carboxyl end (trp) #status experimental

Query Match 36.4%; Score 4; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 L 1  
Db 2 L 2  
RESULT 6  
B44960

neuropeptide Led-CC-II - Colorado potato beetle  
C:Species: Leptinotarsa decemlineata (Colorado potato beetle)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: B44960  
R:Gaede, G.; Kellner, R.  
Peptides 10, 1287-1289, 1989  
A:Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle a  
A:Reference number: A44960; MUID:90160053  
A:Accession: B44960  
A:Molecule type: protein  
A:Residues: 1-8 <GAP>  
C:Superfamily: adipokinetic hormone  
C:Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match 36.4%; Score 4; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 L 1  
Db 2 L 2

RESULT 7  
S15422  
adipokinetic hormone - cockchafer  
N:Alternate names: Melolontha melolontha (cockchafer)  
C:Species: Melolontha melolontha (cockchafer)  
C:Date: 19-Mar-1997 #sequence\_revision 31-Oct-1997 #text\_change 31-Oct-1997  
C:Accession: S15422  
R:Gaede, G.  
Biochem. J. 275, 671-677, 1991  
A:Title: A unique charged tyrosine-containing member of the adipokinetic hormone/red  
A:Reference number: S15422; MUID:91248100  
A:Accession: S15422

A:Molecule type: protein  
 A:Residues: 1-8 <BIO>  
 C:Superfamily: adipokinetic hormone  
 C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 36.4%; Score 4; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1

Db 2 L 2

## RESULT 8

A43976  
 hypertrehalosemic hormone - yellow mealworm  
 C:Species: Tenebrio molitor (yellow mealworm)  
 C:Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 07-May-1999  
 C:Accession: A43976  
 R:Gaede, G.; Rosinski, G.  
 Peptides 11, 455-459, 1990  
 A:Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid beetle  
 A:Reference number: A43976; MUID:90341081  
 A:Accession: A43976  
 A:Molecule type: protein  
 A:Residues: 1-8 <GAE>  
 C:Superfamily: adipokinetic hormone  
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 36.4%; Score 4; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1

Db 2 L 2

## RESULT 9

B43976  
 hypertrehalosemic hormone - beetle (Zophobas rugipes)  
 C:Species: Zophobas rugipes  
 C:Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 07-May-1999  
 C:Accession: B43976  
 R:Gaede, G.; Rosinski, G.  
 Peptides 11, 455-459, 1990  
 A:Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid beetle  
 A:Reference number: A43976; MUID:90341081  
 A:Accession: B43976  
 A:Molecule type: protein  
 A:Residues: 1-8 <GAE>  
 C:Superfamily: adipokinetic hormone  
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 36.4%; Score 4; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1

Db 2 L 2

RESULT 10  
 A33995  
 adipokinetic hormone - black horse fly  
 C:Species: Tabanus atratus (black horse fly)  
 C:Date: 23-Mar-1990 #sequence\_revision 23-Mar-1990 #text\_change 31-Oct-1997  
 C:Accession: A33995  
 R:Jafer, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhan  
 Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989  
 A:Title: Primary structure of two neuropeptide hormones with adipokinetic and hypotretic  
 A:Reference number: A33995; MUID:90046758  
 A:Accession: A33995  
 A:Molecule type: protein  
 A:Residues: 1-8 <JAF>  
 C:Superfamily: adipokinetic hormone  
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted  
 F:8/Modified site: amidated carboxyl end (Trp) #status predicted

Query Match 36.4%; Score 4; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1

Db 2 L 2

## RESULT 11

S11545  
 adipokinetic hormone - nestling-sucking blowfly  
 C:Species: Protophormia terraenovae (nestling-sucking blowfly)  
 C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 31-Oct-1997  
 C:Accession: S11545  
 R:Gaede, G.; Wilps, H.; Kellner, R.  
 Biochem. J. 269, 309-313, 1990  
 A:Title: Isolation and structure of a novel charged member of the red-pigment-concentrating  
 A:Reference number: S11545; MUID:90351345  
 A:Accession: S11545  
 A:Molecule type: protein  
 A:Residues: 1-8 <GAE>  
 C:Superfamily: adipokinetic hormone  
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 36.4%; Score 4; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1

Db 2 L 2

## RESULT 12

A58641  
 adipokinetic hormone - dor beetle  
 C:Species: Geotrupes stercorosus (dor beetle)  
 C:Date: 28-Oct-1997 #sequence\_revision 31-Oct-1997 #text\_change 31-Oct-1997  
 C:Accession: A58641  
 R:Gaede, G.  
 Biochem. J. 275, 671-677, 1991  
 A:Title: A unique charged tyrosine-containing member of the adipokinetic hormone/red  
 A:Reference number: S15422; MUID:91248100  
 A:Accession: A58641  
 A:Molecule type: protein  
 A:Residues: 1-8 <BIO>  
 C:Superfamily: adipokinetic hormone  
 C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 13, 2001, 10:45:38 : Search time 22.81 Seconds  
(Without alignments)  
26.716 Million cell updates/sec

Title: US-09-424-080a-2

Perfect score: 11

Sequence: 1 LXXXXXX 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR,68.\*

1: PIR1.\*

2: PIR2.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	3	2 PQ0010	angiotensin-conver
2	4	36.4	3	2 T13892	cytochrome-c oxida
3	4	36.4	4	2 S18401	thyroglobulin - do
4	4	36.4	4	2 A32039	tyrosine-melanocyt
5	4	36.4	4	2 A48360	gamma subunit of p
6	4	36.4	4	2 B43848	cell surface adhes
7	4	36.4	4	2 I40505	hypothetical prote
8	4	36.4	4	2 T46627	hypothetical prote
9	4	36.4	4	2 I38888	COI intron 16 prot
10	4	36.4	4	2 A35779	neuropeptide Antho
11	4	36.4	4	2 PT0240	Ig heavy chain CRD
12	4	36.4	4	2 A53284	T-cell receptor be
13	4	36.4	4	2 PT0645	T-cell receptor be
14	4	36.4	4	2 PT0731	T-cell receptor be
15	4	36.4	4	2 S47552	ubiquitin - rat
16	4	36.4	4	2 A26209	protein-glutamine
17	4	36.4	5	1 HOROHA	proctolin - Americ
18	4	36.4	5	2 JN0860	peptidyl-dipectida
19	4	36.4	5	2 C41225	copper resistance
20	4	36.4	5	2 S42364	flagellar protein
21	4	36.4	5	2 B22565	R-phycoerythrin al
22	4	36.4	5	2 PQ0009	angiotensin-conver
23	4	36.4	5	2 S55237	zinc-binding prote
24	4	36.4	5	2 A60803	neuropeptide - sea
25	4	36.4	5	2 B61445	Leu-enkephalin - b
26	4	36.4	5	2 A60411	proctolin - Atlant
27	4	36.4	5	2 S53595	hypothetical prote
28	4	36.4	5	2 PT0728	Ig heavy chain CRD
29	4	36.4	5	2 D44823	synaptosomal-assoc

30	4	36.4	5	2 PT0624	T-cell receptor be
31	4	36.4	5	2 PT0625	T-cell receptor be
32	4	36.4	5	2 PT0713	T-cell receptor be
33	4	36.4	5	2 G44817	27.5 kda structura
34	4	36.4	5	2 T44817	27.5K structural p
35	4	36.4	5	2 E44817	27.5K structural p
36	4	36.4	5	2 C44817	28.5K structural p
37	4	36.4	5	2 A44817	28.5K structural p
38	4	36.4	5	2 D44817	34.5K structural p
39	4	36.4	5	2 D44817	35K structural pro
40	4	36.4	5	2 S69237	surface protein ce
41	4	36.4	5	4 A58728	seriawettin W2 - S
42	4	36.4	6	2 A35890	RNA-directed DNA p
43	4	36.4	6	2 B34835	dnaA protein - Pse
44	4	36.4	6	2 A60986	N-formyl oligopept
45	4	36.4	6	2 T11779	phosphoglycerate t

## ALIGNMENTS

RESULT 1  
PQ0010  
angiotensin-converting enzyme inhibitor (FLP-3) - common fig  
N:Alternate names: ficus latex peptide 3  
C:Species: Ficus carica (common fig)  
C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 08-Dec-1995  
C:Accession: PQ0010  
R:Matuyama, S.; Miyoshi, S.; Tanaka, H.  
A:Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.  
A:Reference number: PQ0008  
A:Accession: PQ0010  
A:Molecule type: protein  
A:Residues: 1-3 <MAR>  
A:Experimental source: latex  
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 36.4%; Score 4; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	L	1
DB	1	L	1

RESULT 2  
T13892  
cytochrome-c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey mitochondrion (f  
C:Species: mitochondrion Lampetra fluviatilis (river lamprey)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jul-2000  
C:Accession: T13892  
R:Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Gachelin, G.  
A:Title: The main features of the craniate mitochondrial DNA between the ND1 and the  
Mol. Biol. Evol. 14: 807-813, 1997  
A:Reference number: Z17775; MUID:97398704  
A:Accession: T13892  
A>Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-3 <DEL>  
C:Cross-references: EMBL:Y09528; NID:g2340016; PIDN:CAA70721.1; PID:g4379123  
C:Genetics:  
A:Genome: mitochondrion  
A:Note: COI  
C:Keywords: mitochondrion; oxidoreductase

Query Match 36.4%; Score 4; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
|  
Db 3 L 3

## RESULT 3

S18401  
thyroglobulin - dog (fragment)  
C:Species: Canis lupus familiaris (dog)  
C:Date: 19-Mar-1997 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
C:Accession: S18401  
R:Donda, A.; Vassart, G.; Christophe, D.  
Biochim. Biophys. Acta 1090, 235-237, 1991  
A:Title: Isolation and characterization of the canine thyroglobulin gene promoter region  
A:Reference number: S18401; MUID:92031697  
A:Accession: S18401  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-4 <DON>  
A:Cross-references: GB:S61184; NID:9237714; PID:9237715  
C:Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat homology  
C:Keywords: duplication; iodine; thyroid gland; thyroid hormone biosynthesis

Query Match 36.4%; Score 4; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
|  
Db 3 L 3

## RESULT 4

A32039  
tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 31-Jul-1989 #sequence\_revision 31-Jul-1989 #text\_change 18-Aug-2000  
C:Accession: A32039  
R:Horvath, A.; Kastin, A.J.  
J. Biol. Chem. 264, 2175-2179, 1989  
A:Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor  
A:Reference number: A32039; MUID:89123285  
A:Accession: A32039  
A:Molecule type: protein  
A:Residues: 1-4 <HOR>  
A:Experimental source: brain  
C:Superfamily: unassigned animal peptides  
C:Keywords: amidated carboxyl end  
F:4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 36.4%; Score 4; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
|  
Db 3 L 3

## RESULT 5

A48360  
gamma subunit of Protein A - Methylosinus trichosporium (fragment)  
C:Species: Methylosinus trichosporium  
C:Date: 19-Nov-1993 #sequence\_revision 18-Nov-1994 #text\_change 08-Oct-1999  
C:Accession: A48360  
R:Cardy, D.L.; Laidler, V.; Salmund, G.P.; Murrell, J.C.  
Arch. Microbiol. 156, 477-483, 1991  
A:Title: The methane monooxygenase gene cluster of Methylosinus trichosporium: cloning and characterization  
A:Reference number: A48360; MUID:92153031  
A:Contents: OR3B  
A:Accession: A48360

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-4 <CAR>  
A:Cross-references: GB:S81887; NID:9245213; PID:9245214  
A:Note: sequence extracted from NCBI backbone (NCBI:81887, MCBIP:81912)

Query Match 36.4%; Score 4; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
|  
Db 2 L 2

## RESULT 6

B43848  
cell surface adhesin for heparan sulfate, 60K - Staphylococcus aureus (fragment)  
C:Species: Staphylococcus aureus  
C:Date: 10-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 24-Feb-1995  
C:Accession: B43848  
R:Liang, O.D.; Ascencio, F.; Fransson, L.A.; Wadstrom, T.  
Infect. Immun. 60, 899-906, 1992  
A:Title: Binding of heparan sulfate to Staphylococcus aureus.  
A:Reference number: A43848; MUID:92176005  
A:Accession: B43848  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-4 <LIA>  
A:Note: sequence extracted from NCBI backbone (NCBI:85444)

Query Match 36.4%; Score 4; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
|  
Db 2 L 2

## RESULT 7

I40505  
hypothetical protein 3 (4 aa) - Bacillus stearothermophilus  
C:Species: Bacillus stearothermophilus  
C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 15-Oct-1999  
C:Accession: I40505  
R:Waye, M.M.; Winter, G.  
Eur. J. Biochem. 158, 505-510, 1986  
A:Title: A transcription terminator in the 5' non-coding region of the tyrosyl tRNA synthetase gene  
A:Reference number: I40503; MUID:86274732  
A:Accession: I40505  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-4 <RES>  
A:Cross-references: EMBL:X04193; NID:940233; PID:CAA27783.1; PID:9580944

Query Match 36.4%; Score 4; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
|  
Db 2 L 2

## RESULT 8

t46627  
hypothetical protein c4 - loblolly pine  
C:Species: Pinus taeda (loblolly pine)  
C:Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 18-Feb-2000

C:Accession: T46627  
 R:Chang, S.; Puryear, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.  
 submitted to the EMBL Data Library, July 1995  
 A:Description: Cloning of a chitinase homolog which lacks chitin binding sites and is de  
 A:Reference number: 223105  
 A:Accession: T46627  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-4 <CH>  
 A:Cross-references: EMBL:U31309; NID:9974295; PID:974292  
 A:Experimental source: strain 967236PT3; 8 month seedlings

Query Match 36.4%; Score 4; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 |  
 Db 3 L 3

## RESULT 9

I38888  
 COI Intron 16 protein - Podospora anserina mitochondrion  
 C:Species: mitochondrion Podospora anserina  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-Dec-1999  
 C:Accession: I38888  
 R:Cummings, D.J.; Michel, F.; McNally, K.L.  
 Curr. Genet. 16: 381-406, 1989  
 A:Title: DNA sequence analysis of the 24.5 kilobase pair cytochrome oxidase subunit I m  
 A:Reference number: A48327; MUID:90124722  
 A:Accession: I38888  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-4 <CUM>  
 A:Cross-references: GB:X55096; GB:M30937; GB:M61734  
 C:Genetics:  
 A:Genome: mitochondrion  
 A:Genetic code: SGC3  
 C:Keywords: mitochondrion

Query Match 36.4%; Score 4; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 |  
 Db 2 L 2

## RESULT 10

A35779  
 neuropeptide Antho-RNamide - sea anemone (Anthopleura elegantissima)  
 C:Species: Anthopleura elegantissima  
 C:Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 08-Dec-1995  
 C:Accession: A35779  
 R:Grimmelikhuijzen, C.J.P.; Rinehart, K.L.; Jacob, E.; Graff, D.; Reinscheid, R.K.; Not  
 Proc. Natl. Acad. Sci. U.S.A. 87, 5410-5414, 1990  
 A:Title: Isolation of L-3-phenylacetyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea anemone ne  
 A:Reference number: A35779; MUID:90319122  
 A:Accession: A35779  
 A:Molecule type: protein  
 A:Residues: 1-4 <GRI>  
 C:Comment: The L-3-phenylacetyl blocking group probably arises from an amino-terminal ph  
 C:Keywords: amidated carboxyl end; neuropeptide; phenylacetylation  
 F.1/Modified site: L-3-phenylacetyl acid (Phe) #status experimental  
 F.4/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 36.4%; Score 4; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 L 1  
 |  
 Db 2 L 2  
 RESULT 11  
 PT0240  
 Ig heavy chain CRD3 region (clone 2-100B) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C:Accession: PT0240  
 R:Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an  
 A:Reference number: PT0222; MUID:91108337  
 A:Accession: PT0240  
 A:Molecule type: DNA  
 A:Residues: 1-4 <YAM>  
 A:Experimental source: B lymphocyte  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 36.4%; Score 4; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 |  
 Db 4 L 4

## RESULT 12

A53284  
 T-cell receptor beta 2 chain D region, Dbeta2 - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
 C:Accession: A53284  
 R:Harindranath, N.; Alexander, C.B.; Mage, R.G.  
 Mol. Immunol. 28, 881-888, 1991  
 A:Title: Evolutionarily conserved organization and sequences of germline diversity an  
 A:Reference number: A53284; MUID:91342695  
 A:Accession: A53284  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-4 <HAR>  
 A:Cross-references: GB:S60737; NID:9233916; PID:AA819517.1; PID:9233917  
 A:Note: Sequence extracted from NCBI backbone (NCBI:60737, NCBI:60739)  
 C:Keywords: T-cell receptor

Query Match 36.4%; Score 4; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 |  
 Db 2 L 2

## RESULT 13

PT0645  
 T-cell receptor beta chain V-D-J region (111-1A1) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PT0645; PT0626  
 R:Penney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions  
 A:Reference number: PT0509; MUID:91277601  
 A:Accession: PT0645  
 A:Status: translation not shown

Search completed: December 13, 2001, 10:45:38  
Job time: 58 sec

A: Molecule type: mRNA  
A: Residues: 1-4 <FE2>  
A: Experimental source: newborn thymus, strain BALB/c, 111-1A1  
A: Accession: PT0626  
A: Status: translation not shown  
A: Molecule type: mRNA  
A: Residues: 1-4 <FE2>  
A: Experimental source: newborn thymus, strain BALB/c, 120-2CJ  
A: Keywords: T-cell receptor

Query Match 36.4%; Score 4; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
Db 4 L 4

## RESULT 14

PT0721  
T-cell receptor beta chain V-D-J region (140-2K) - mouse (fragment)  
C: Species: Mus musculus (house mouse)  
C: Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C: Accession: PT0721  
R: Feeney, A. J.  
J. Exp. Med. 174, 115-124, 1991  
A: Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A: Reference number: PT0509; MUID: 91277601  
A: Accession: PT0721  
A: Status: translation not shown  
A: Molecule type: DNA  
A: Residues: 1-4 <FE2>  
A: Experimental source: newborn thymus, strain BALB/c  
A: Keywords: T-cell receptor

Query Match 36.4%; Score 4; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
Db 3 L 3

## RESULT 15

S47552  
ubiquitin - rat  
C: Species: Rattus norvegicus (Norway rat)  
C: Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 17-Mar-1999  
C: Accession: S47552  
R: Hubbard, M. J.; Carne, A.  
Biochim. Biophys. Acta 1200, 191-196, 1994  
A: Title: Differential feeding-related regulation of ubiquitin and calbindin(9kDa) in rat  
A: Reference number: S47552; MUID: 94304928  
A: Accession: S47552  
A: Status: preliminary  
A: Molecule type: protein  
A: Residues: 1-4 <HUB>

Query Match 36.4%; Score 4; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
Db 1 L 1

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 13, 2001, 10:50:49 ; Search time 12.78 seconds  
(without alignments)  
22.951 Million cell updates/sec

Title: US-09-424-080A-2

Perfect score: 11

Sequence: 1 LXXXXXX 8

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	36.4	4	1 FAR3_HIRME	P42562 hirudo medi
2	4	36.4	4	1 FLRF_HIRME	P42561 hirudo medi
3	4	36.4	5	1 ALL4_CARMA	P81817 carcinus ma
4	4	36.4	5	1 PRCT_PRRAM	P01373 periplaneta
5	4	36.4	6	1 ACPIH_RABIT	P25154 oryctolagus
6	4	36.4	6	1 TMOF_SARBU	P41495 sarcophaga
7	4	36.4	6	1 TRPI_PSEPU	P36414 pseudomonas
8	4	36.4	6	1 VP19_HSV1K	P23210 herpes simp
9	4	36.4	7	1 ALL2_CARMA	P81805 carcinus ma
10	4	36.4	7	1 ALL3_CARMA	P81806 carcinus ma
11	4	36.4	7	1 ALL4_CARMA	P81807 carcinus ma
12	4	36.4	7	1 ALL5_CARMA	P81808 carcinus ma
13	4	36.4	7	1 ALL7_CYDPO	P82158 cydia pomon
14	4	36.4	7	1 CARP_MTEED	P20420 mytilus edu
15	4	36.4	7	1 CCF1_ENTFA	P20104 enterococcu
16	4	36.4	7	1 C1A_ENTFA	P11932 enterococcu
17	4	36.4	7	1 FARI_HELTI	P41871 helisoma tr
18	4	36.4	7	1 FARI_PROCL	P38499 procambartu
19	4	36.4	7	1 FAR2_PROCL	P31890 ascaris suu
20	4	36.4	7	1 FAR2_PROCL	P38498 procambartu
21	4	36.4	7	1 GFPR_MOUSE	P99025 mus musculu
22	4	36.4	7	1 MNPI_LRPDE	P42984 leptinotars
23	4	36.4	7	1 MYOM_APLCA	P15513 aplysia cal
24	4	36.4	7	1 UF03_MOUSE	P38641 mus musculu
25	4	36.4	7	1 UN06_PINPS	P81675 pinus pinas
26	4	36.4	8	1 AKH_MELML	P25423 melolontha
27	4	36.4	8	1 AKH_TABAT	P14595 tabanus atr
28	4	36.4	8	1 AL12_CARMA	P81815 carcinus ma
29	4	36.4	8	1 AL13_CARMA	P81816 carcinus ma
30	4	36.4	8	1 AL15_CARMA	P81818 carcinus ma
31	4	36.4	8	1 AL17_CARMA	P81819 carcinus ma
32	4	36.4	8	1 AL18_CARMA	P81820 carcinus ma
33	4	36.4	8	1 ALL1_CYDPO	P82152 cydia pomon

34	4	36.4	8	1 ALL3_CYDPO	P82154 cydia pomon
35	4	36.4	8	1 ALL4_CALVO	P41840 calliophora
36	4	36.4	8	1 ALL4_CYDPO	P82155 cydia pomon
37	4	36.4	8	1 ALL5_CYDPO	P82156 cydia pomon
38	4	36.4	8	1 ALL6_CYDPO	P82157 cydia pomon
39	4	36.4	8	1 ALL7_CARMA	P81809 carcinus ma
40	4	36.4	8	1 ALL8_CARMA	P81811 carcinus ma
41	4	36.4	8	1 ALL9_CARMA	P81812 carcinus ma
42	4	36.4	8	1 COX1_ENTFA	P3268 enterococcu
43	4	36.4	8	1 COXG_RAT	P80430 rattus norv
44	4	36.4	8	1 CPD1_ENTFA	P13269 enterococcu
45	4	36.4	8	1 NPB_BOVIN	P15507 bos taurus

## ALIGNMENTS

RESULT 1  
FAR3\_HIRME  
ID FAR3\_HIRME STANDARD: PRT; 4 AA.  
AC P42562;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE FMRFAMIDE-LIKE NEUROPEPTIDE YLRP-AMIDE.  
OS Hirudo medicinalis (Medicinal leech).  
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
OC Arynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.  
OX NCBI\_TaxID=6421;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92195954; PubMed=1686933;  
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
RT "Identification of Remamide neuropeptides in the medicinal leech."  
RL Peptides 12:897-908(1991).  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 4 4  
SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;  
AMIDATION.

Query Match 36.4%; Score 4; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
Db 2 L 2

RESULT 2  
FLRF\_HIRME  
ID FLRF\_HIRME STANDARD: PRT; 4 AA.  
AC P42561;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE FMRFAMIDE.  
OS Hirudo medicinalis (Medicinal leech), and Helisoma trivolvis (Snail).  
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
OC Arynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.  
OX NCBI\_TaxID=6421, 27815;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=H. medicinalis;  
RX MEDLINE=92195954; PubMed=1686933;  
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
RT "Identification of Remamide neuropeptides in the medicinal leech."  
RL Peptides 12:897-908(1991).  
CC [2]  
KW Neuropeptide.  
FT MOD\_RES 4 4  
SQ SPECIES=H. trivolvis; TISSUE=Kidney;

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RX MEDLINE-94286417; PubMed-7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRamide-related peptides from the kidney of the snail, Helisoma
RL trivolvis.";
CC Peptides 15:31-36(1994).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4 4
SQ SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;

Query Match 36.4%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1
Db 2 L 2

RESULT 3
ID AL14_CARMA STANDARD; PRT; 5 AA.
AC P81617.
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE CARCINOSTATIN 14.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE-98121193; PubMed-9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and Identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- SIMILARITY: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 5 5
SQ SEQUENCE 5 AA; 586 MW; 672875D5AB300000 CRC64;

Query Match 36.4%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1
Db 5 L 5

RESULT 4
ID PCT_PERAM STANDARD; PRT; 5 AA.
AC P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE PROCTOLIN.
OS Periplaneta americana (American cockroach),
OS Limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.

RX MEDLINE-94286417; PubMed-7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRamide-related peptides from the kidney of the snail, Helisoma
RL trivolvis.";
CC Peptides 15:31-36(1994).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4 4
SQ SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;

Query Match 36.4%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1
Db 3 L 3

RESULT 5
ID ACPH_RABIT STANDARD; PRT; 6 AA.
AC P25154;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ACYLAMINO-ACID-RELEASING ENZYME (EC 3.4.19.1) (ACYL-PEPTIDE HYDROLASE)
DE (APH) (ACYLAMINOACYL-PEPTIDASE) (FRAGMENT).
GN APEH.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE-92222120; PubMed-1807161;
RA Krishna R.G., Chin C.C.O., Wolf F.;
RT "N-terminal sequence analysis of N alpha-acetylated proteins after

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RT unblocking with N-acetylaminocetyl-peptide hydrolase.";  
 RL Anal. Biochem. 199:45-50(1991).  
 CC -!- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-  
 CC TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE  
 CC AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.  
 CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.  
 CC -!- CATALYTIC ACTIVITY: ACYLAMINOACYL-PEPTIDE + H(2)O -> ACYLAMINO  
 CC ACID + PEPTIDE.  
 CC -!- SUBUNIT: HOMOTETRAMER.  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C; ALSO KNOWN AS THE  
 CC PROLYL OLIGOPEPTIDASE FAMILY.  
 CC MEROPS: S09.004;  
 DR InterPro: IPR002471; Prol.endopep\_ser.  
 DR PROSITE: PS00708; PRO-ENDOPEP\_SER; PARTIAL.  
 KW Hydrolase; Acetylation.  
 FT MOD\_RES 1 1 ACETYLATION.  
 FT NON\_TER 6 6  
 SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;

Query Match 36.4%; Score 4; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1

Db 6 L 6

RESULT 6

ID TMOF SARBUB STANDARD; PRT; 6 AA.  
 AC P41493;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE TRYPsin-MODULATING OOSTATIC FACTOR (TMOF).  
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Oestroidea; Sarcophagidae; Sarcophaga.  
 CC NCBI\_TaxID=7385;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE-Ovary;  
 RX MEDLINE=94211930; PubMed=8159807;  
 RA Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,  
 RA de Loof A.;  
 RT "Sequencing and characterization of trypsin modulating oostatic  
 RT factor (TMOF) from the ovaries of the grey fleshfly, Neobellieria  
 RT (Sarcophaga) bullata.";  
 RL Regul. Pept. 50:61-72(1994).  
 CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS  
 CC IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN  
 CC CONCENTRATION IN THE HEMOLYMPH RESULTING IN INHIBITION OF OOCYTE  
 CC DEVELOPMENT.  
 CC -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR  
 CC EPITHELIUM AFTER A BLOOD MEAL.  
 KW Hormone.  
 SQ SEQUENCE 6 AA; 695 MW; 61E72451B7642000 CRC64;

Query Match 36.4%; Score 4; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1

Db 5 L 5

RESULT 7

TRPI\_PSEPU

ID TRPI\_PSEPU STANDARD; PRT; 6 AA.  
 AC P36414;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE TRPB OPERON TRANSCRIPTIONAL ACTIVATOR (FRAGMENT).  
 CC TRPI.  
 OS Pseudomonas putida.  
 CC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 CC Pseudomonas.  
 CC NCBI\_TaxID=303;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PGI C1S;  
 RX MEDLINE=89335826; PubMed=2503057;  
 RT Eberly L., Crawford I.P.;  
 RT "DNA sequence of the tryptophan synthase genes of Pseudomonas  
 RT putida.";  
 RL Biochimie 71:521-531(1989).  
 CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPB GENES ENCODING  
 CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE  
 CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE  
 CC TRPB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.  
 CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL  
 CC REGULATORS.  
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 CC EMBL; X13299; CAA31660.1;  
 DR InterPro: IPR000847; HTH\_LYSR.  
 DR PROSITE: PS00044; HTH\_LYSR\_FAMILY; PARTIAL.  
 KW Tryptophan biosynthesis; Transcription regulation; Activator;  
 KW DNA-binding.  
 FT NON\_TER 6 6  
 SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;

Query Match 36.4%; Score 4; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 Db 5 L 5

RESULT 8  
 ID VP19\_HSVIK STANDARD; PRT; 6 AA.  
 AC P23210;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 01-DEC-1992 (Rel. 24, Last annotation update)  
 DE CAPSID ASSEMBLY AND DNA MATURATION PROTEIN (VIRION PROTEIN UL38)  
 DE (CAPSID PROTEIN VP19C) (FRAGMENT).  
 GN UL38.  
 OS Herpes simplex virus (type 1 / strain KOS).  
 CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 CC Alphaherpesvirinae; Simplexvirus.  
 CC NCBI\_TaxID=10306;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91101287; PubMed=1846198;  
 RA Flanagan W.M., Papavasiliou A.G., Rice M., Hecht L.B.,  
 RA Silverstein S., Wagner E.K.;  
 RT "Analysis of the herpes simplex virus type 1 promoter controlling the  
 RT expression of UL38, a true late gene involved in capsid assembly.";



RL J. Virol. 65:769-786(1991).  
 CC -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSID ARE  
 CC EMBEDDED. BINDS DNA.  
 CC -!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M57646; AAA45830.1; -  
 DR Capsid assembly; Coat protein; DNA-binding.  
 KW NON\_TER 6  
 FT SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;  
 SQ

Query Match 36.4%; Score 4; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 Db 6 L 6

## RESULT 9

ALL3\_CARMA STANDARD; PRT; 7 AA.  
 ID ALL3\_CARMA  
 AC P81805;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE CARCINUSTATIN 2.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 CC Eubranchyura; Portunoidae; Portunidae; Carcinus.  
 CC NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RT Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas.";  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 CC Neuropeptide; Multigene family.  
 FT MOD\_RES 7  
 SQ SEQUENCE 7 AA; 770 MW; 672879CDBC5DBD70 CRC64;

Query Match 36.4%; Score 4; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 Db 7 L 7

## RESULT 10

ALL3\_CARMA STANDARD; PRT; 7 AA.  
 ID ALL3\_CARMA  
 AC P81806;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE CARCINUSTATIN 3.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 CC Eubranchyura; Portunoidae; Portunidae; Carcinus.  
 CC NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RT Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas.";  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 CC Neuropeptide; Multigene family.  
 SQ SEQUENCE 7 AA; 796 MW; 672879CDBC476B70 CRC64;

Query Match 36.4%; Score 4; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 Db 7 L 7

## RESULT 11

ALL4\_CARMA STANDARD; PRT; 7 AA.  
 ID ALL4\_CARMA  
 AC P81807;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE CARCINUSTATIN 4.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 CC Eubranchyura; Portunoidae; Portunidae; Carcinus.  
 CC NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RT Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas.";  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 CC Neuropeptide; Multigene family.  
 SQ SEQUENCE 7 AA; 782 MW; 672879CDBC476AC0 CRC64;

Query Match 36.4%; Score 4; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 Db 7 L 7

## RESULT 12

ALL5\_CARMA STANDARD; PRT; 7 AA.  
 ID ALL5\_CARMA  
 AC P81808;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE CARCINUSSTATIN 5.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunoidea; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 allatostatin superfamily in the shore crab Carcinus maenas.";  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -!- FUNCTION: MAY ACT AS A NEUROTROPHIC OR NEUROMODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD\_RES 7  
 SQ SEQUENCE 7 AA; 781 MW; 672879CDBA76420 CRC64;

Query Match 36.4%; Score 4; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 Db 7 L 7

RESULT 13  
 ALL7 CYDPO STANDARD; PRT; 7 AA.  
 AC 882158; 2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE CYDIASTATIN 7.  
 OS Cydia pomonella (Codling moth).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 OX NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 Davey M., East P.D., Thorpe A.;  
 RT "Lepidopteran peptides of the allatostatin superfamily";  
 RL Peptides 18:1301-1309(1997).  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 7  
 SQ SEQUENCE 7 AA; 873 MW; 672879CABB569350 CRC64;

Query Match 36.4%; Score 4; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 Db 7 L 7

RESULT 14  
 CARR\_MYTED STANDARD; PRT; 7 AA.  
 AC P10420;  
 DT 01-MAR-1989 (Rel. 10, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 01-MAR-1989 (Rel. 10, Last annotation update)  
 DE CATCH-RELAXING PEPTIDE (CARP).  
 OS Mytilus edulis (Blue mussel).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
 OC Mytiloidea; Mytilidae; Mytilus.  
 OX NCBI\_TaxID=6550;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=88052022; PubMed=3676797;  
 RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,  
 Muneoka Y.;  
 RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia";  
 RL Brain Res. 422:374-376(1987).  
 CC -!- FUNCTION: THIS PEPTIDE EXHIBITS BOTH POTENTIATING (CONTRACTION)  
 CC AND INHIBITORY (RELAXATION) EFFECTS ON THE ANTERIOR BYSSUS  
 CC RETRACTOR MUSCLE.  
 CC PIR: A29342; ECMUCR.  
 DR Hormone; Amidation.  
 KW MOD\_RES 7  
 FT SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;

Query Match 36.4%; Score 4; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 Db 5 L 5

RESULT 15  
 CCF1\_ENTFA STANDARD; PRT; 7 AA.  
 AC P20104;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last annotation update)  
 DE SEX PHEROMONE CCF10.  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;  
 OC Enterococcus.  
 OX NCBI\_TaxID=1351;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=89008313; PubMed=3139658;  
 RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,  
 Adsit J.C., Dunny G.M., Suzuki A.;  
 RT "Structure of cCF10, a peptide sex pheromone which induces  
 conjugative transfer of the Streptococcus faecalis tetracycline  
 resistance plasmid, pCF10";  
 RL J. Biol. Chem. 263:14574-14578(1988).  
 CC -!- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE  
 CC HEMOLYSIN PLASMID PCF10.  
 CC PIR: A30812; A30812.  
 DR Pheromone.  
 KW SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;

Query Match 36.4%; Score 4; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 Db 1 L 1

Search completed: December 13, 2001, 10:50:49  
 Job time: 308 sec



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RESULT 2
Q08720
ID O08720 PRELIMINARY; PRT; 6 AA.
AC O08720
DT 01-NOV-1996 (TREMREL. 01, Created)
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
DT 01-NOV-1996 (TREMREL. 08, Last annotation update)
DE Y PROTEIN (FRAGMENT).
GN CREB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93010691; PubMed=1396344;
RA Waeber G., Habener J.F.;
RT *Novel testis germ cell-specific transcript of the CREB gene contains
RT an alternatively spliced exon with multiple in-frame stop codons.*;
RL Endocrinology 131:2010-2015(1992).
DR EMBL; X68994; CAA48780.1;
FT NON_TER 1
FT NON_TER 6
SQ SEQUENCE 6 AA; 695 MW; 67272EB9C735D000 CRC64;

Query Match 36.4%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1
Db 2 L 2

RESULT 3
P82541
ID P82541 PRELIMINARY; PRT; 6 AA.
AC P82541
DT 01-OCT-2000 (TREMREL. 15, Created)
DT 01-OCT-2000 (TREMREL. 15, Last sequence update)
DT 01-JUN-2001 (TREMREL. 17, Last annotation update)
DE CHLOROPLAST 30S RIBOSOMAL PROTEIN S19 BETA (FRAGMENT).
OS Spinacia oleracea (Spinach).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RX STRAIN=CV. ALMARO; TISSUE=LEAF;
RX MEDLINE=20435797; PubMed=10874039;
RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
RT The plastid ribosomal proteins. Identification of all the proteins in
RT the small subunit of an organelle ribosome (chloroplast).;
RL J. Biol. Chem. 274:28455-28465(2000).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -1- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
CC -1- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.
CC -1- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PL. S19 BETA
CC FORM IS THE MINOR BASIC FORM.
CC -1- MISCELLANEOUS: ON THE 2D-GEL, ITS MW IS: 12 KDA.
CC -1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro: IPR002222; RiboSomaL_S19.
DR Pfam: PF00303; RiboSomaL_S19; PARTIAL.
DR PRINTS: PR00975; RIBOSOMALS19; PARTIAL.
DR PROSITE: PS00323; RIBOSOMALS19; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER 6

SQ SEQUENCE 6 AA; 695 MW; 67272EB9C735D000 CRC64;

Query Match 36.4%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1
Db 2 L 2

RESULT 4
O54248
ID O54248 PRELIMINARY; PRT; 7 AA.
AC O54248
DT 01-NOV-1996 (TREMREL. 01, Created)
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
DT 01-NOV-1996 (TREMREL. 01, Last annotation update)
DE SECY & ADK GENES (FRAGMENT).
GN RPLO.
OS Streptomyces griseus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1911;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=N2-3-11;
RA Poehling S., Piepersberg W., Wehmeier U.F.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X5915; CAA65160.1;
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 7 AA; 760 MW; 72C72B01B2D1B2A0 CRC64;

Query Match 36.4%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1
Db 6 L 6

RESULT 5
O07354
ID O07354 PRELIMINARY; PRT; 7 AA.
AC O07354
DT 01-JUL-1997 (TREMREL. 04, Created)
DT 01-JUL-1997 (TREMREL. 04, Last sequence update)
DT 01-AUG-1998 (TREMREL. 07, Last annotation update)
DE NIFK (FRAGMENT).
GN NIFK.
OS Synchococcus sp. (strain PCC 8801 / RF-1) (Cyanothecae PCC 8801).
OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
OX NCBI_TaxID=41431;
RN [1]
RP SEQUENCE FROM N.A.
RX CHEN H.M.;
RA CHEN H.M.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003700; AAC35193.1;
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 7 AA; 849 MW; 7412C72AA9D5B030 CRC64;

Query Match 36.4%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1
Db 5 L 5

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RESULT 6
ID O50556 PRELIMINARY; PRT; 7 AA.
AC O50556;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE GLYA (FRAGMENT).
GN GLYA.
OS Actinobacillus actinomycetemcomitans (Haemophilus
actinomycetemcomitans);
OC Bacteria, Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Actinobacillus.
OX NCBI_TaxID=714;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 3384;
RX MEDLINE=96355846; PubMed=8751884;
RA Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,
RA Kraig E.;
RT *cis Elements and trans factors are both important in strain-specific
RT regulation of the leukotoxin gene in Actinobacillus
RT actinomycetemcomitans.
RL Infect. Immun. 64:3451-3460(1996).
DR EMBL; U51862; AAB88721.1; -
FT NON_TER 1
SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;

Query Match 36.4%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 L 1
Db 3 L 3

RESULT 7
ID Q15897 PRELIMINARY; PRT; 7 AA.
AC Q15897;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE (CLONE XP6A11A) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
RA Caskey C.T.H.;
RL Hum. Mol. Genet. 0:0-0(0).
DR EMBL; L32077; AAA73887.1; -
FT NON_TER 1
FT NON_TER 7
SQ SEQUENCE 7 AA; 814 MW; 672B1DD3372046B0 CRC64;

Query Match 36.4%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 L 1
Db 3 L 3

RESULT 8
ID P92421 PRELIMINARY; PRT; 7 AA.
AC P92421; P92419;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-JAN-1998 (TREMBlrel. 05, Last annotation update)
DE RIBOSOMAL PROTEIN 11 (FRAGMENT).
GN RPS11.
OS Psathyrostachys fragilis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Psathyrostachys.
OX NCBI_TaxID=37729;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H4372, AND H917; TISSUE=LEAVES;
RA Petersen G., Seberg O.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z77753; CAB01337.1; -
DR EMBL; Z77752; CAB01334.1; -
FT NON_TER 1
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 36.4%; Score 4; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 L 1
Db 7 L 7

RESULT 9
ID P92385 PRELIMINARY; PRT; 7 AA.
AC P92385; P92383;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-JAN-1998 (TREMBlrel. 05, Last annotation update)
DE RIBOSOMAL PROTEIN 11 (FRAGMENT).
GN RPS11.
OS Hordeum marinum (Seaside barley).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H299, AND H801; TISSUE=LEAVES;
RA Petersen G., Seberg O.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z77763; CAB01367.1; -
DR EMBL; Z77762; CAB01364.1; -
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 36.4%; Score 4; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 L 1
Db 7 L 7

```

RESULT 10  
 ID P92210 PRELIMINARY; PRT; 7 AA.  
 AC P92210;  
 DT 01-MAY-1997 (TREMELREL. 03, Created)  
 DE 01-MAY-1997 (TREMELREL. 03, Last sequence update)  
 DT 01-AUG-1998 (TREMELREL. 07, Last annotation update)  
 DE RIBOSOMAL PROTEIN 11 (FRAGMENT).  
 GN RPS11.  
 OS Australopyrum retrofractum.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Agropyron.  
 OX NCBI\_TaxID=4593;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-H4349; TISSUE-LEAVES;  
 RA Petersen G., Seberg O.;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; 277771; CAB01391.1; -  
 KW Ribosomal protein; Chloroplast.  
 FT NON\_TER 1  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 36.4%; Score 4; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 I  
 Db 7 L 7

RESULT 11  
 ID P92214 PRELIMINARY; PRT; 7 AA.  
 AC P92214;  
 DT 01-MAY-1997 (TREMELREL. 03, Created)  
 DE 01-MAY-1997 (TREMELREL. 03, Last sequence update)  
 DT 01-AUG-1998 (TREMELREL. 07, Last annotation update)  
 DE RIBOSOMAL PROTEIN 11 (FRAGMENT).  
 GN RPS11.  
 OS Amblyopyrum muticum.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Amblyopyrum.  
 OX NCBI\_TaxID=4595;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-H5572; TISSUE-LEAVES;  
 RA Petersen G., Seberg O.;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; 277756; CAB01346.1; -  
 KW Ribosomal protein; Chloroplast.  
 FT NON\_TER 1  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 36.4%; Score 4; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 I  
 Db 7 L 7

RESULT 12  
 ID P92218 PRELIMINARY; PRT; 7 AA.

P92218;  
 AC 01-MAY-1997 (TREMELREL. 03, Created)  
 DT 01-MAY-1997 (TREMELREL. 03, Last sequence update)  
 DE 01-AUG-1998 (TREMELREL. 07, Last annotation update)  
 DE RIBOSOMAL PROTEIN 11 (FRAGMENT).  
 GN RPS11.  
 OS Australopyrum retrofractum.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Australopyrum.  
 OX NCBI\_TaxID=4597;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-H6723; TISSUE-LEAVES;  
 RA Petersen G., Seberg O.;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; 277767; CAB01379.1; -  
 KW Ribosomal protein; Chloroplast.  
 FT NON\_TER 1  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 36.4%; Score 4; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 I  
 Db 7 L 7

RESULT 13  
 ID P92221 PRELIMINARY; PRT; 7 AA.  
 AC P92221;  
 DT 01-MAY-1997 (TREMELREL. 03, Created)  
 DE 01-MAY-1997 (TREMELREL. 03, Last sequence update)  
 DT 01-AUG-1998 (TREMELREL. 07, Last annotation update)  
 DE RIBOSOMAL PROTEIN 11 (FRAGMENT).  
 GN RPS11.  
 OS Bromus inermis (Smooth brome grass).  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Bromaceae; Bromus.  
 OX NCBI\_TaxID=15371;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-OSA414; TISSUE-LEAVES;  
 RA Petersen G., Seberg O.;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; 277759; CAB01355.1; -  
 KW Ribosomal protein; Chloroplast.  
 FT NON\_TER 1  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 36.4%; Score 4; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 I  
 Db 7 L 7

RESULT 14  
 ID P92226 PRELIMINARY; PRT; 7 AA.

AC P92226;  
 DT 01-MAY-1997 (TREMELREL. 03, Created)  
 DT 01-MAY-1997 (TREMELREL. 03, Last sequence update)

Thu Dec 13 10:55:22 2001

01-AUG-1998 (TREMBLrel. 07, Last annotation update)  
 DE RIBOSOMAL PROTEIN 11 (FRAGMENT).  
 GN RPS11  
 OS Crittropsis delileana.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Crittropsis.  
 OX NCBI\_TaxID=37674;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN-H5561; TISSUE-LEAVES;  
 RA Petersen G.; Seberg O.;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; 277751; CAB01301.1; -  
 KW Ribosomal protein; Chloroplast.  
 FT NON\_TER 1  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 36.4%; Score 4; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 Db 7 L 7

RESULT 15  
 ID P92372 PRELIMINARY; PRT; 7 AA.  
 AC P92372;  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)  
 DE RIBOSOMAL PROTEIN 11 (FRAGMENT).  
 GN RPS11.  
 OS Haynaldia villosa.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;  
 OC Panicoideae; Andropogoneae; Haynaldia.  
 OX NCBI\_TaxID=40247;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN-H5561; TISSUE-LEAVES;  
 RA Petersen G.; Seberg O.;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; 277741; CAB01301.1; -  
 KW Ribosomal protein; Chloroplast.  
 FT NON\_TER 1  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 36.4%; Score 4; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 Db 7 L 7

Search completed: December 13, 2001, 10:50:31  
 Job time: 320 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 13, 2001, 10:46:23 ; Search time 38.61 Seconds  
(without alignments)  
15.348 Million cell updates/sec

Title: US-09-424-080a-2  
Perfect score: 11  
Sequence: 1 LXXXXXX 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_1101.\*  
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5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
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21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	36.4	2	21	AA844925
2	4	36.4	2	21	AA827827
3	4	36.4	2	22	AA899717
4	4	36.4	2	22	AA891562
5	4	36.4	2	22	AA891740
6	4	36.4	2	22	AA891749
7	4	36.4	3	10	AA893533
8	4	36.4	3	10	AA893348
9	4	36.4	3	10	AA890667
10	4	36.4	3	11	AA870737
11	4	36.4	3	11	AA8707580

12	4	36.4	3	12	AA810543
13	4	36.4	3	14	AA838486
14	4	36.4	3	14	AA839998
15	4	36.4	3	14	AA859412
16	4	36.4	3	15	AA865950
17	4	36.4	3	15	AA846817
18	4	36.4	3	15	AA848960
19	4	36.4	3	15	AA849510
20	4	36.4	3	15	AA851439
21	4	36.4	3	15	AA851440
22	4	36.4	3	15	AA851441
23	4	36.4	3	15	AA858569
24	4	36.4	3	15	AA858570
25	4	36.4	3	15	AA858571
26	4	36.4	3	16	AA875205
27	4	36.4	3	16	AA882733
28	4	36.4	3	16	AA882737
29	4	36.4	3	16	AA882744
30	4	36.4	3	16	AA882919
31	4	36.4	3	16	AA884432
32	4	36.4	3	16	AA864398
33	4	36.4	3	16	AA864689
34	4	36.4	3	16	AA864624
35	4	36.4	3	16	AA864624
36	4	36.4	3	17	AA898823
37	4	36.4	3	17	AA898825
38	4	36.4	3	17	AA898826
39	4	36.4	3	17	AA898827
40	4	36.4	3	17	AA898828
41	4	36.4	3	17	AA898828
42	4	36.4	3	17	AA898898
43	4	36.4	3	18	AA831319
44	4	36.4	3	18	AA831314
45	4	36.4	3	21	AA879636

## ALIGNMENTS

RESULT 1  
ID AAB44925 standard; Protein; 2 AA.  
AC AAB44925;  
XX 12-FEB-2001 (first entry)  
DE Human secreted protein encoded by gene 9.  
XX Secreted protein; human; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; gene therapy; treatment; autoimmune disease; infection; cardiovascular disorder; nervous system disorder; ocular disorder; wound healing; epithelial cell proliferation; skin aging; mental state; transplantation; metabolism modulation.  
XX Homo sapiens.  
XX WO200055200-A1.  
XX 21-SEP-2000.  
XX 09-MAR-2000; 2000WO-US06042.  
XX 12-MAR-1999; 99US-0124143.  
XX 03-DEC-1999; 99US-0168663.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Rosen CA, Ruben SM, Komatsoulis G.  
XX WPI; 2000-656008/63.

Hypotensive oligop  
Human RDS Pro216Le  
Scintigraph imagin  
Angiotensin conver  
Tripeptide inhibit  
Phyts derived pe  
NLA-3 truncated GA  
Endothelin antago  
IGF-1 analogue N-t  
IGF-1 analogue N-t  
Angiotensin I conv  
Angiotensin I conv  
Angiotensin I conv  
Microbial emetic t  
Apolipoprotein A-I  
Apolipoprotein A-I  
Apolipoprotein A-I  
Non-RGD, non-YISGR  
Non-RGD, non-YISGR  
DP-178 homologue 3  
DP-178 homologue 1  
HPF3 peptide deriv  
HPF3 peptide deriv  
Active domain from  
Mutant chemokine a  
Mutant chemokine a  
Active domain from  
Small synthetic an  
Human Interleukin-  
Human Interleukin-  
Peroxisome reactan





(SMIK ) SMITHKLINE BEECHAM PLC.

Lupas AN, Pearce KH;

WPI; 2001-476108/51.

New ERA binding domain polypeptides and polynucleotides encoding them, useful as research reagents and materials for discovery of treatments and diagnostics for diseases, or for genetic immunisation.

Claim 1; Page 26; 279pp; English.

The present invention relates to ERA binding domain polypeptides (AAG9559-AAG9989 and AAM0010-AAM00021). The era gene in Escherichia coli codes for an essential GTPase protein able to autophosphorylate at serine and/or threonine residues. The protein has potential antimicrobial and antibacterial activity and is useful in screening for antagonists, agonists and for compounds with antibiotic activity. The proteins are also useful in determining their role in pathogenesis of infection, dysfunction and disease and could be used as part of a vaccine and/or peptide therapy.

Sequence 2 AA;

Query Match 36.4%; Score 4; DB 22; Length 2;

Best Local Similarity 100.0%; Pred. No. 3.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1

DB 1 1 1

RESULT 4

AAB91562 ID AAB91562 standard; Peptide: 2 AA.

AC AAB91562;

DT 22-JUN-2001 (first entry)

DE Endothelins and related peptides SEQ ID NO:738.

KW Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.

PN WO200069900-A2.

PD 23-NOV-2000.

PE 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

WPI; 2001-112059/12.

Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure; Page 438; 733pp; English.

XX

CC The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptide stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.

Sequence 2 AA;

Query Match 36.4%; Score 4; DB 22; Length 2;

Best Local Similarity 100.0%; Pred. No. 3.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1

DB 1 1 1

RESULT 5

AAB91740 ID AAB91740 standard; Peptide: 2 AA.

AC AAB91740;

DT 22-JUN-2001 (first entry)

DE Opioid peptide SEQ ID NO:916.

KW Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.

PN WO200069900-A2.

PD 23-NOV-2000.

PE 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

WPI; 2001-112059/12.

Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure; Page 492; 733pp; English.

XX

CC The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently

XX

CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity  
 CC in vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention.  
 SQ Sequence 2 AA;

Query Match 36.4%; Score 4; DB 22; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 DB 1 1 1

RESULT 6  
 ID AAB91749 standard; Peptide; 2 AA.

XX AAB91749;  
 XX 22-JUN-2001 (first entry)  
 XX Opioid peptide SEQ ID NO:925.  
 XX Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 XX blood component; modification; succinimidyl; maleimido group; amino;  
 XX hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
 XX Homo sapiens.  
 XX Synthetic.  
 XX WO200069900-A2.  
 XX 23-NOV-2000.  
 XX 17-MAY-2000; 2000WO-US13576.  
 XX 17-MAY-1999; 99US-0134406.  
 XX 10-SEP-1999; 99US-0153406.  
 XX 13-OCT-1999; 99US-0159783.  
 XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaut K;  
 XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents  
 XX peptidase degradation, useful for increasing length of in vivo activity

XX Disclosure; Page 495; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)  
 XX comprising a therapeutically active amino acid region (III) and a  
 XX reactive group (II) (e.g. succinimidyl and maleimido groups) attached to  
 XX a less therapeutically active amino acid region (IV), which covalently  
 XX bonds with amino/hydroxyl/thiol groups on blood components to form a  
 XX peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 XX (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 XX factors and neurotransmitters, to protect them from peptidase activity

CC in vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention.  
 SQ Sequence 2 AA;

Query Match 36.4%; Score 4; DB 22; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 DB 2 1 2

RESULT 7  
 ID AAP93533 standard; protein; 3 AA.

XX AAP93533;  
 XX 06-JUN-1990 (first entry)  
 XX N-terminal portion of the leader peptide of the heavy chain variable  
 XX region (VH) gene as encoded in T15.  
 XX Mammalian immunoglobulin; mammalian T-cell receptor;  
 XX chimeric polypeptide; TEPC 15VH; heavy chain variable region; T15 VH;  
 XX anti-tumour activity; MMULV-LTR; MMULV-LTR-VH.

XX JP01063394-A.

XX 09-MAR-1989.

XX 04-SEP-1987; 87JP-0221758.

XX 04-SEP-1987; 87JP-0221758.

XX (FUJI-) FUJITA GAKUEN GH (KYOW).

XX WPI; 1989-118256/16.

XX N-PSDB; AAN92384.

XX New chimeric polypeptide having antitumour activity -  
 XX contains variable region of mammalian immunoglobulin and  
 XX constant region of mammalian T-cell receptor

XX Disclosure; page 23 (2); 29pp; Japanese.

XX The coding sequence for the H chain variable region (VH) in TEPC 15VH,  
 XX and MMULV-LTR were subcloned in order to prepare MMULV-LTR-VH, as part of  
 XX the process of preparing a new chimeric polypeptide containing the  
 XX variable region of mammalian immunoglobulin and the constant region of  
 XX mammalian T-cell receptor. The chimeric polypeptide is expected to confer  
 XX anti-tumour activity on cells.

XX Sequence 3 AA;

Query Match 36.4%; Score 4; DB 10; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 DB 3 1 3



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Thu Dec 13 10:55:17 2001

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RESULT 11
AAR07580
ID AAR07580 standard; peptide; 3 AA.
XX
AC AAR07580;
XX
DT 08-FEB-1991 (first entry)
XX
DE Hypotensive polypeptide.
XX
KW Gamma-casein.
XX
OS Zea mays.
XX
PN JP02240027-A.
XX
PD 25-SEP-1990.
XX
PF 14-MAR-1989; 89JP-0059549.
XX
PR 14-MAR-1989; 89JP-0059549.
XX
PA (AGEN ) AGENCY OF IND SCI TECH.
XX
PA (SHOS ) SHOWA KK.
XX
DR WPI; 1990-332335/44.
XX
XX New polypeptide hypotensive agents - are tri-, penta- or
PT hexa-peptide(s) derived from gamma casein
XX
PS Claim 1; Page 193; 5pp; Japanese.
XX
CC Peptide, derived from Zea mays gamma-casein, is useful as an anti-
CC hypotensive agent in mammals and humans.
XX
SQ Sequence 3 AA;

Query Match 36.4%; Score 4; DB 11; Length 3;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1
Db 1 1 1

RESULT 12
AAR10543
ID AAR10543 standard; Protein; 3 AA.
XX
AC AAR10543;
XX
DT 15-MAR-1991 (first entry)
XX
DE Hypotensive oligopeptide.
XX
KW Oral hypotensive; fig.
XX
OS Ficus carica.
XX
PN JP02282394-A.
XX
PD 19-NOV-1990.
XX
PF 24-APR-1989; 89JP-0104265.
XX
PR 24-APR-1989; 89JP-0104265.
XX
PA (AGEN ) AGENCY OF IND SCI TECH.
XX
PA (SHOS ) SHOWA SANGYO KK.
XX

Query Match 36.4%; Score 4; DB 11; Length 3;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1
Db 1 1 1

RESULT 13
AAR38486
ID AAR38486 standard; Protein; 3 AA.
XX
AC AAR38486;
XX
DT 11-NOV-1993 (first entry)
XX
DE Human RDS Pro216Leu fragment.
XX
KW Human; mutant; retinal degeneration; primer; rds; photoreceptor;
KW hereditary; retinitis pigmentosa; amplify; retina; murine; autosomal;
KW dominant; PCR.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 2
FT /note= "Pro216Leu"
PN W09312134-A.
XX
PD 24-JUN-1993.
XX
PF 08-DEC-1992; 92WO-US10536.
XX
PR 11-DEC-1991; 91US-0805123.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI Berson EL, Dryja TP;
XX
DR WPI; 1993-214088/26.
XX
DR N-PSDB; AAQ43555.
XX
PT Probe or primer contg. sequence of human retinal degeneration
PT slow protein mutant - used to diagnose hereditary retinal
PT degenerative diseases
XX
PS Disclosure; Fig 13B; 56pp; English.
XX
XX The sequences given in AAR38485-87 represent regions of the human
XX retinal degeneration slow (RDS) protein which contain mutations.
XX These mutations of the human RDS protein cosegregate with autosomal
XX dominant retinitis pigmentosa. The RDS gene sequence was isolated
XX via the murine rds gene and has been mapped to chromosome 6p. The
XX murine rds gene is a semidominant mutation with a phenotype of
XX abnormal development of rod and cone photoreceptors, followed by
XX their slow degeneration. The DNA encoding the mutation containing
XX regions was isolated by polymerase chain reaction (PCR) using primers
XX derived from RDS gene intron flanking sequences.

```



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 13, 2001, 10:45:08 ; Search time 19.94 seconds  
(without alignments)  
9.028 Million cell updates/sec

Title: US-09-424-080A-2  
Perfect score: 11  
Sequence: 1 LXXXXXX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents RA:\*

- 1: /cgn2\_6/ptodata/2/iaa/5A-COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B-COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A-COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B-COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/iaa/PCRTUS-COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	4	36.4	2	2	US-08-451-822A-19
2	4	36.4	2	2	US-08-915-414A-6
3	4	36.4	2	3	US-09-039-308A-4
4	4	36.4	3	1	US-07-663-413-7
5	4	36.4	3	1	US-07-663-413-10
6	4	36.4	3	1	US-07-840-077A-3
7	4	36.4	3	1	US-07-947-035-3
8	4	36.4	3	1	US-07-947-035-4
9	4	36.4	3	1	US-08-055-530-7
10	4	36.4	3	1	US-08-055-530-10
11	4	36.4	3	1	US-08-082-853-2
12	4	36.4	3	1	US-08-081-539-117
13	4	36.4	3	1	US-08-221-582A-2
14	4	36.4	3	1	US-08-167-336A-3
15	4	36.4	3	1	US-08-466-641-117
16	4	36.4	3	1	US-08-288-681A-6
17	4	36.4	3	1	US-08-305-768-26
18	4	36.4	3	1	US-08-411-389-20
19	4	36.4	3	1	US-08-213-897A-9
20	4	36.4	3	1	US-08-213-897A-10
21	4	36.4	3	1	US-08-179-481-116
22	4	36.4	3	1	US-08-179-984-2
23	4	36.4	3	1	US-08-416-962-3
24	4	36.4	3	1	US-08-321-585A-1
25	4	36.4	3	1	US-08-321-585A-2
26	4	36.4	3	1	US-08-321-585A-3
27	4	36.4	3	1	US-08-321-585A-4

28	4	36.4	3	1	US-08-464-456-25
29	4	36.4	3	1	US-08-454-950-3
30	4	36.4	3	1	US-08-634-060-36
31	4	36.4	3	1	US-08-338-282-11
32	4	36.4	3	1	US-08-741-678-6
33	4	36.4	3	1	US-08-406-192-45
34	4	36.4	3	1	US-08-589-011-3
35	4	36.4	3	1	US-08-269-929-2
36	4	36.4	3	1	US-08-454-949-3
37	4	36.4	3	1	US-08-153-848-17
38	4	36.4	3	1	US-08-443-675-2
39	4	36.4	3	1	US-08-447-010-17
40	4	36.4	3	1	US-08-445-206-2
41	4	36.4	3	1	US-07-923-724-44
42	4	36.4	3	1	US-08-843-035-30
43	4	36.4	3	1	US-08-463-052-25
44	4	36.4	3	1	US-08-470-837-7
45	4	36.4	3	4	US-09-383-630-9

## ALIGNMENTS

RESULT 1  
US-08-451-822A-19  
; Sequence 19, Application US/08451822A  
; Patent No. 5863888  
; GENERAL INFORMATION:  
; APPLICANT: Dionne, Craig A  
; APPLICANT: Crumley, Greg  
; APPLICANT: Jaye, Michael C  
; APPLICANT: Schlessinger, Joseph  
; TITLE OF INVENTION: Fibroblast Growth Factor Receptors  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Roter Legal Department  
; STREET: 500 Accola Road  
; CITY: Collegeville  
; STATE: PA USA  
; COUNTRY: USA  
; ZIP: 19426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/451,822A  
; APPLICATION NUMBER: US/08/451,822A  
; FILING DATE: 26-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/323,430  
; FILING DATE: 14-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/934,372  
; FILING DATE: 21-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/549,587  
; FILING DATE: 06-JUL-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Savitzky, Martin  
; REGISTRATION NUMBER: 29,699  
; REFERENCE/DOCKET NUMBER: A0496E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610) 454-3816  
; TELEFAX: (610) 454-3808  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-451-822A-19

Query Match 36.4%; Score 4; DB 2; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
 Db 2 L 2

## RESULT 2

US-08-915-414A-6  
 ; Sequence 6, Application US/08915414A  
 ; Patent No. 5976822  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LANDRUM, ET AL.  
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR MONITORING APOPTOSIS  
 ; AND DISTINGUISHING APOPTOSIS FROM NECROSIS  
 ; NUMBER OF SEQUENCES: 6  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: MITCHELL, ALTER, COULTER INTERN. CORP.  
 ; STREET: 11800 SW 147 AVE.  
 ; CITY: MIAMI  
 ; STATE: FLORIDA  
 ; COUNTRY: USA  
 ; ZIP: 33196  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage  
 ; COMPUTER: IBM PC  
 ; OPERATING SYSTEM: MS-DOS  
 ; SOFTWARE: Microsoft Word 6.0/95  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/915,414A  
 ; FILING DATE: 20-AUG-1997  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/444,051  
 ; FILING DATE: 18-MAY-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: MITCHELL E. ALTER  
 ; REGISTRATION NUMBER: 28,684  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (305) 380-3636  
 ; TELEFAX: (305) 380-4566  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-915-414A-6

Query Match 36.4%; Score 4; DB 2; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
 Db 1 L 1

## RESULT 3

US-09-039-308A-4  
 ; Sequence 4, Application US/09039308A  
 ; Patent No. 6069129  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sandberg, Lawrence; Roos, Phillip;  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mitts, Thomas  
 ; REGISTRATION NUMBER: ELASTIN DERIVED COMPOSITION

;; TITLE OF INVENTION: AND METHOD OF  
 ;; TITLE OF INVENTION: USING SAME  
 ;; NUMBER OF SEQUENCES: 41  
 ;; CORRESPONDENCE ADDRESS:  
 ;; ADDRESSEE: REED SMITH SHAW & MCCRAY, LLP  
 ;; STREET: PO Box 488  
 ;; CITY: Pittsburgh  
 ;; STATE: Pennsylvania  
 ;; COUNTRY: USA  
 ;; ZIP: 15230  
 ;; COMPUTER READABLE FORM:  
 ;; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb  
 ;; COMPUTER: Compaq  
 ;; OPERATING SYSTEM: Microsoft Windows 95  
 ;; SOFTWARE: Word 6.0  
 ;; CURRENT APPLICATION DATA:  
 ;; APPLICATION NUMBER: US/09/039,308A  
 ;; FILING DATE: March 13, 1998  
 ;; CLASSIFICATION: 514  
 ;; ATTORNEY/AGENT INFORMATION:  
 ;; NAME: Miller, Raymond A.  
 ;; REGISTRATION NUMBER: 42,891  
 ;; REFERENCE/DOCKET NUMBER: 97-489  
 ;; TELECOMMUNICATION INFORMATION:  
 ;; TELEPHONE: (412) 288-4192  
 ;; TELEFAX: (412) 288-1300  
 ;; INFORMATION FOR SEQ ID NO: 4:  
 ;; SEQUENCE CHARACTERISTICS:  
 ;; LENGTH: 2 amino acids  
 ;; TYPE: amino acid  
 ;; STRANDEDNESS: single  
 ;; TOPOLOGY: linear  
 ;; MOLECULE TYPE: peptide  
 ;; US-09-039-308A-4

Query Match 36.4%; Score 4; DB 3; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
 Db 1 L 1

RESULT 4  
 US-07-663-413-7  
 ; Sequence 7, Application US/07663413  
 ; Patent No. 5240703  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cochran, Mark D.  
 ; TITLE OF INVENTION: ATTENUATED, GENETICALLY-ENGINEERED  
 ; PSEUDORABIES VIRUS S-PRV-155 AND USE THEREOF  
 ; NUMBER OF SEQUENCES: 32  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: John P. White, Esq.  
 ; STREET: 30 Rockefeller Plaza  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10112  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.24  
 ; CURRENT APPLICATION DATA:  
 ;; APPLICATION NUMBER: US/07/663,413  
 ;; FILING DATE: 19910301  
 ;; CLASSIFICATION: 424  
 ;; ATTORNEY/AGENT INFORMATION:  
 ;; NAME: White Esq., John P.  
 ;; REGISTRATION NUMBER: 28,678



us-09-424-080a-2.open.rai

Thu Dec 13 10:55:18 2001

REFERENCE/DOCKET NUMBER: 38720  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 7  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-663-413-7

Query Match 36.4%; Score 4; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

QY 1 L 1  
DB 2 L 2

RESULT 5  
US-07-663-413-10  
Sequence 10, Application US/07663413  
Patent No. 5240703  
GENERAL INFORMATION:  
APPLICANT: Cochran, Mark D.  
TITLE OF INVENTION: ATTENUATED, GENETICALLY-ENGINEERED  
PSEUDORABIES VIRUS S-PRV-155 AND USE THEREOF  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White, Esq.  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/663,413  
FILING DATE: 19910301  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: White Esq., John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 38720  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 10  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-663-413-10

Query Match 36.4%; Score 4; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

QY 1 L 1  
DB 2 L 2

RESULT 6  
US-07-840-077A-3  
Sequence 3, Application US/07840077A  
Patent No. 5443816  
GENERAL INFORMATION:  
APPLICANT: zamora, Paul O.  
APPLICANT: Rhodes, Buck A.  
TITLE OF INVENTION: Peptide-Metal Ion  
Pharmaceutical Preparation and Method  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhomed Incorporated  
STREET: 4261 Balloon Park  
CITY: Albuquerque  
STATE: NM  
COUNTRY: U.S.A.  
ZIP: 87109-5802  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB  
MEDIUM TYPE: Storage  
COMPUTER: IBM PC/XT/AT, IBM PS/2 or  
COMPATIBLES  
OPERATING SYSTEM: PC-DOS or MS-DOS  
SOFTWARE: Wordperfect 6.0a for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/840,077A  
FILING DATE: 20-FEB-1992  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/816,477  
FILING DATE: 03-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Deborah A. Peacock  
REGISTRATION NUMBER: 31,649  
TELEPHONE: (505) 242-9677  
TELEFAX: (505) 243-2542  
INFORMATION FOR SEQ ID NO: 3  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
US-07-840-077A-3

Query Match 36.4%; Score 4; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

QY 1 L 1  
DB 2 L 2

RESULT 7  
US-07-947-035-3  
Sequence 3, Application US/07947035  
Patent No. 5444045  
GENERAL INFORMATION:  
APPLICANT: Francis, Geoffrey L.  
APPLICANT: Walton, Paul E.  
APPLICANT: Ballard, Francis J.  
APPLICANT: McMurty, John P.  
APPLICANT: Phelps, Patricia V.  
TITLE OF INVENTION: Method of Administering IGF-1, IGF-2,  
and Analogs Thereof to Birds  
NUMBER OF SEQUENCES: 18

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Kenneth D. Sibley  
;; STREET: P.O. Drawer 34009  
;; CITY: Charlotte  
;; STATE: No. 5444045th Carolina  
;; COUNTRY: US  
;; ZIP: 28234  
;;  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent in Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/947,035  
;; FILING DATE: 17-SEP-1992  
;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sibley, Kenneth D.  
;; REGISTRATION NUMBER: 31,665  
;; REFERENCE/DOCKET NUMBER: 5175-59  
;; TELEPHONE: (919) 881-3140  
;; TELEFAX: (919) 881-3175  
;; TELEX: 575102  
;;  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 3 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
;;  
;; US-07-947-035-3

Query Match 36.4%; Score 4; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
Db 2 L 2

RESULT 8  
US-07-947-035-4  
; Sequence 4, Application US/07947035  
; Patent No. 5444045  
; GENERAL INFORMATION:  
; APPLICANT: Francis, Geoffrey L.  
; APPLICANT: Walton, Paul E.  
; APPLICANT: Ballard, Francis J.  
; APPLICANT: McMurty, John P.  
; APPLICANT: Phelps, Patricia V.  
; TITLE OF INVENTION: Method of Administering IGF-1, IGF-2,  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kenneth D. Sibley  
; STREET: P.O. Drawer 34009  
; CITY: Charlotte  
; STATE: No. 5444045th Carolina  
; COUNTRY: US  
; ZIP: 28234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/947,035  
; FILING DATE: 17-SEP-1992  
; CLASSIFICATION: 514

;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sibley, Kenneth D.  
;; REGISTRATION NUMBER: 31,665  
;; REFERENCE/DOCKET NUMBER: 5175-59  
;; TELEPHONE: (919) 881-3140  
;; TELEFAX: (919) 881-3175  
;; TELEX: 575102  
;;  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 3 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
;;  
;; US-07-947-035-4

Query Match 36.4%; Score 4; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
Db 2 L 2

RESULT 9  
US-07-947-035-5  
; Sequence 5, Application US/07947035  
; Patent No. 5444045  
; GENERAL INFORMATION:  
; APPLICANT: Francis, Geoffrey L.  
; APPLICANT: Walton, Paul E.  
; APPLICANT: Ballard, Francis J.  
; APPLICANT: McMurty, John P.  
; APPLICANT: Phelps, Patricia V.  
; TITLE OF INVENTION: Method of Administering IGF-1, IGF-2,  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kenneth D. Sibley  
; STREET: P.O. Drawer 34009  
; CITY: Charlotte  
; STATE: No. 5444045th Carolina  
; COUNTRY: US  
; ZIP: 28234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/947,035  
; FILING DATE: 17-SEP-1992  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sibley, Kenneth D.  
; REGISTRATION NUMBER: 31,665  
; REFERENCE/DOCKET NUMBER: 5175-59  
; TELEPHONE: (919) 881-3140  
; TELEFAX: (919) 881-3175  
; TELEX: 575102  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO

us-09-424-080a-2.open.rai

Thu Dec 13 10:55:18 2001

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US-07-947-035-5
Query Match          36.4%; Score 4; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1
Db 2 L 2

RESULT 10
US-08-055-530-7
; Sequence 7, Application US/08055530
; Patent No. 5451499
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: ATTENUATED, GENETICALLY-ENGINEERED
; TITLE OF INVENTION: PSEUDORABIES VIRUS S-PRV-155 AND USES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/055,530
; FILING DATE: 19930430
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 38720-Z/JPW/JEL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-055-530-7

Query Match          36.4%; Score 4; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1
Db 2 L 2

RESULT 12
US-08-082-853-2
; Sequence 2, Application US/08082853
; Patent No. 5496718
; GENERAL INFORMATION:
; APPLICANT: HASHIMOTO, NOBUKAZU
; APPLICANT: KOCHIZUKI, HIDEO
; APPLICANT: HAMAI, AKIO
; APPLICANT: ISHIKAWA, SHINICHI
; APPLICANT: TORIKAI, MISAOKO
; APPLICANT: MIYACHI, ISAO
; TITLE OF INVENTION: CHONDROITINASE, PROCESS FOR PREPARING
; TITLE OF INVENTION: THE SAME, AND PHARMACEUTICAL COMPOSITION COMPRISING THE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,853
; FILING DATE: 19930623
; US-08-055-530-10
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;
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL ESQ. PAULA A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: 3999/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7263
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1-3
; OTHER INFORMATION: /note= "C-terminal sequence of
; OTHER INFORMATION: Chondroitinase ABC"
; US-08-082-853-2

Query Match 36.4%; Score 4; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
Db 2 L 2

RESULT 13
US-08-081-539-117
; Sequence 117, Application US/08081539
; Patent No. 5501962
; GENERAL INFORMATION:
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olins, Peter O.
; TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine
; TITLE OF INVENTION: Chimeric Hybrid Polypeptides
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate
; ADDRESSEE: Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/081,539
; FILING DATE: 19930621
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanady, Mary J.
; REGISTRATION NUMBER: 28623
; REFERENCE/DOCKET NUMBER: 2724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708)470-6501
; TELEFAX: (708)470-6881
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-081-539-117

Query Match 36.4%; Score 4; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
Db 2 L 2

RESULT 14
US-08-221-582A-2
; Sequence 2, Application US/08221582A
; Patent No. 5505946
; GENERAL INFORMATION:
; APPLICANT: Ann R. Kennedy, Bernard F. Szuhaaj
; TITLE OF INVENTION: Bowman-Birk Inhibitor Concentrate
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Pre-Malignant
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,582A
; FILING DATE: April 1, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,335
; FILING DATE: No. 5505946ember 2, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: UPSC-0027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-221-582A-2

Query Match 36.4%; Score 4; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
Db 2 L 2

RESULT 15
US-08-167-336A-3
; Sequence 3, Application US/08167336A
; Patent No. 5531990
; GENERAL INFORMATION:
; APPLICANT: THANAVALA, YASMIN
; APPLICANT: THAKUR, ARVIND
```

us-09-424-080a-2.open.ra

Thu Dec 13 10:55:18 2001

APPLICANT: ROITT, IVAN  
 APPLICANT: PRIDE, MICHAEL  
 TITLE OF INVENTION: ANTI-IDIOTYPIC ANTIBODY  
 TITLE OF INVENTION: HAVING CORRESPONDENCE WITH HUMAN HEPATITIS  
 TITLE OF INVENTION: B SURFACE ANTIGEN  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: DUNN & ASSOCIATES, P.C.  
 STREET: P.O. BOX 96  
 CITY: NEWFANE  
 STATE: NEW YORK  
 COUNTRY: USA  
 ZIP: 14108  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB  
 COMPUTER: VICTOR 300 SX/25  
 OPERATING SYSTEM: MS-DOS VERSION 5.0  
 SOFTWARE: WORDSTAR PROFESSIONAL RELEASE 4  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/167,336A  
 FILING DATE: 15-DEC-1993  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: DUNN, MICHAEL L  
 REGISTRATION NUMBER: 25,330  
 REFERENCE/DOCKET NUMBER: RPP-138 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (716) 433-1661  
 TELEFAX: (716) 433-1665  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3  
 TYPE: AMINO ACID  
 STRANDEDNESS: UNKNOWN  
 TOPOLOGY: UNKNOWN  
 MOLECULE TYPE: PEPTIDE  
 HYPOTHETICAL: NO  
 ANTI-SENSE:  
 FRAGMENT TYPE:  
 ORIGINAL SOURCE:  
 ORGANISM:  
 STRAIN:  
 INDIVIDUAL ISOLATE:  
 DEVELOPMENTAL STAGE:  
 HAPLOTYPE:  
 TISSUE TYPE:  
 CELL TYPE:  
 CELL LINE:  
 ORGANELLE:  
 IMMEDIATE SOURCE:  
 LIBRARY:  
 CLONE:  
 POSITION IN GENOME:  
 CHROMOSOME/SEGMENT:  
 MAP POSITION:  
 UNITS:  
 FEATURE:  
 NAME/KEY:  
 LOCATION:  
 IDENTIFICATION METHOD:  
 OTHER INFORMATION:  
 PUBLICATION INFORMATION:  
 AUTHORS:  
 TITLE:  
 JOURNAL:  
 VOLUME:  
 ISSUE:  
 PAGES:  
 DATE:  
 DOCUMENT NUMBER:

FILING DATE:  
 PUBLICATION DATE:  
 RELEVANT RESIDUES IN SEQ ID NO:  
 US-08-167-336A-3  
 Query Match 36.4%; Score 4; DB 1; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 L 1  
 Db 2 L 2  
 Search completed: December 13, 2001, 10:45:09  
 Job time: 29 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 13, 2001, 12:01:34 ; Search time 12.48 Seconds  
(without alignments)  
23.503 Million cell updates/sec

Title: US-09-424-080A-2

Perfect score: 11  
Sequence: 1 LXXXXXXX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 64

Minimum DB seq length: 8  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	36.4	8	AKH_MEI.L	P15423 melolontha
2	4	36.4	8	AKH_TABAT	P14595 tabanus atr
3	4	36.4	8	AL12_CARNA	P81815 carclinus ma
4	4	36.4	8	AL15_CARNA	P81818 carclinus ma
5	4	36.4	8	AL16_CARNA	P81819 carclinus ma
6	4	36.4	8	AL17_CARNA	P81820 carclinus ma
7	4	36.4	8	AL18_CARNA	P81821 carclinus ma
8	4	36.4	8	AL13_CYDPO	P82152 cydia pomon
9	4	36.4	8	AL14_CYDPO	P82154 cydia pomon
10	4	36.4	8	AL14_CALVO	P41840 calliphora
11	4	36.4	8	AL15_CYDPO	P82155 cydia pomon
12	4	36.4	8	AL16_CYDPO	P82157 cydia pomon
13	4	36.4	8	AL17_CARNA	P81809 carclinus ma
14	4	36.4	8	AL18_CARNA	P81811 carclinus ma
15	4	36.4	8	AL19_CARNA	P81812 carclinus ma
16	4	36.4	8	CAD1_ENTFA	P13368 entrococcu
17	4	36.4	8	CAD1_ENTFA	P80430 rattus norv
18	4	36.4	8	CPD1_ENTFA	P13369 entrococcu
19	4	36.4	8	CPD1_ENTFA	P13372 panagrellu
20	4	36.4	8	FAR1_PANRE	P41486 homarus ame
21	4	36.4	8	FAR3_HOMAM	P41487 homarus ame
22	4	36.4	8	FAR2_HOMAM	P41488 homarus ame
23	4	36.4	8	HTF2_PERAM	P23419 periplaneta
24	4	36.4	8	HTF2_PERAM	P23420 periplaneta
25	4	36.4	8	HTF2_PERAM	P23421 periplaneta
26	4	36.4	8	HTF2_PERAM	P23422 periplaneta
27	4	36.4	8	HTF2_PERAM	P23423 periplaneta
28	4	36.4	8	HTF2_PERAM	P23424 periplaneta
29	4	36.4	8	HTF2_PERAM	P23425 periplaneta
30	4	36.4	8	HTF2_PERAM	P23426 periplaneta
31	4	36.4	8	HTF2_PERAM	P23427 periplaneta
32	4	36.4	8	HTF2_PERAM	P23428 periplaneta
33	4	36.4	8	HTF2_PERAM	P23429 periplaneta

34	2	18.2	8	1	ALL5_CALVO	P41841 calliphora
35	2	18.2	8	1	ANG2_BOTJA	O10582 bothriops ja
36	2	18.2	8	1	B44K_PORGI	P81886 porphyromen
37	2	18.2	8	1	CCKN_MACCU	P30359 macroopus eu
38	2	18.2	8	1	FAR7_ASCSU	P43171 ascaris stu
39	2	18.2	8	1	FAR8_CALVO	P41863 calliphora
40	2	18.2	8	1	FUSS_FUSSO	P81010 fusarium so
41	2	18.2	8	1	PLF_BRANA	P81707 brassica na
42	2	18.2	8	1	RS10_SALTY	O68928 salmoneilla
43	2	18.2	8	1	VGLG_HSV2B	P81780 herpes simp
44	2	18.2	8	1	AKHG_GRYBI	P14086 gryllus dim
45	1	9.1	8	1	AKH_LIBAU	P25418 libellula a

## ALIGNMENTS

RESULT	1	STANDARD	PRT	8 AA
AKH_MEI.L				
ID	AKH_MEI.L			
AC	P25423			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	01-FEB-1994 (Rel. 28, Last annotation update)			
DE	ADIPOKINETIC HORMONE (AKH)			
OS	Melolontha melolontha (Cockchafer)			
OS	Geotrupes stercoreus (Dor beetle)			
OC	Pachnoda marginata (Flower beetle)			
OC	Eukariyota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;			
OC	Scarabaeiformia; Scarabaeidae; Melolonthinae; Melolontha.			
OX	NCBI_TaxID=7061, 7087, 7058;			
RN	[1]			
RP	SEQUENCE.			
RC	SPECIES=M.melolontha, and G.stercoreus; TISSUE=Corpora cardiaca;			
RX	MEDLINE=91248100; Pubmed=2039445;			
RA	Gaele G.;			
RT	"A unique charged tyrosine-containing member of the adipokinetic			
RT	hormone/red-pigment-concentrating hormone peptide family isolated and			
RT	sequenced from two beetle species."			
RL	Biochem. J. 275:671-677(1991).			
RN	[2]			
RP	SEQUENCE.			
RC	SPECIES=P.marginalia; TISSUE=Corpora cardiaca;			
RX	MEDLINE=92265187; Pubmed=1586453;			
RA	Gaele G., Lopata A., Kellner R., Rinehart K.L. Jr.;			
RT	"Primary structures of neuropeptides isolated from the corpora			
RT	cardiaca of various cetonoid beetle species determined by			
RT	pulsed-liquid phase sequencing and tandem fast atom bombardment mass			
RT	spectrometry."			
RL	Biol. Chem. Hoppe-Seyler 373:133-142(1992).			
CC	-1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA			
CC	CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF			
CC	DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT			
CC	MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.			
CC	-1- SIMILARITY: BELONGS TO THE AKH / HTH / RECH FAMILY.			
DR	PIR: S15422; S15422.			
DR	PIR: S21663; S21663.			
DR	Interpro: IP002047; AKH.			
DR	PROSITE: PS00256; AKH; 1.			
KW	Neuropeptide; Amidation; Flight.			
FT	MOD RES	1	8	PYRROLIDONE CARBOXYLIC ACID.
FT	MOD RES	8	8	AMIDATION.
FT	SEQUENCE	8 AA; 1022 MW; 867AB75AB544736 CRC64;		
OY	1 L 1	36.4%; Score 4; DB 1; Length 8;		
DB	2 L 2	Best Local Similarity 100.0%; Pred. No. 0;		
		Matches -1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		

RESULT 2  
AKH\_TABAT STANDARD: PRT: 8 AA.  
ID AKH\_TABAT  
AC P14595;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-FEB-1994 (Rel. 28, Last annotation update)  
DE ADIPOKINETIC HORMONE (AKH) (DIPTERAN CORPORA CARDIACA FACTOR I)  
DE (DCC I).  
OS Tabanus atratus (Horse fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Tabanomorpha;  
OC Tabanidae; Tabanus.  
OX NCBI\_TaxID=7207;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Corpora cardiaca; PubMed-2813385;  
RX MEDLINE=90046758; PubMed-2813385;  
RA Valde H., Raina A.K., Riley C.T., Fraser B.A., Neelman R.J.,  
Vogel V.W., Zhang L.S., Hayes D.K.;  
RT Primary structure of two neuropeptide hormones with adipokinetic and  
RT hypotrehalosemic activity isolated from the corpora cardiaca of horse  
RT flies (Diptera).  
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).  
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA  
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF  
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT  
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.  
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RCH FAMILY.  
DR PIR: A33995; A33995.  
DR InterPro: IPR02047; AKH.  
DR PROSITE: PS00256; AKH; 1.  
KW Neuropeptide; Amidation; flight.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA: 949 MW: 86786771A9D1A736 CRC64;  
  
Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 L 1  
DB 2 L 2  
  
RESULT 3  
AL12\_CARMA STANDARD: PRT: 8 AA.  
ID AL12\_CARMA  
AC P81815;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE CARCINOSTATIN 12.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed-9461295;  
RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
Thorepe A.;  
RT Isolation and identification of multiple neuropeptides of the  
RT allatostatin superfamily in the shore crab Carcinus maenas.";  
RT Eur. J. Biochem. 250:727-734(1997).  
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.

KW Neuropeptide; Multigene family.  
SQ SEQUENCE 8 AA: 913 MW: 672879C0CB569AB7 CRC64;  
  
Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 L 1  
DB 8 L 8  
  
RESULT 4  
AL15\_CARMA STANDARD: PRT: 8 AA.  
ID AL15\_CARMA  
AC P81818;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE CARCINOSTATIN 15.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed-9461295;  
RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
Thorepe A.;  
RT Isolation and identification of multiple neuropeptides of the  
RT allatostatin superfamily in the shore crab Carcinus maenas.";  
RT Eur. J. Biochem. 250:727-734(1997).  
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation; Multigene family.  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA: 811 MW: 922879D5AB47687D CRC64;  
  
Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 L 1  
DB 8 L 8  
  
RESULT 5  
AL16\_CARMA STANDARD: PRT: 8 AA.  
ID AL16\_CARMA  
AC P81819;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE CARCINOSTATIN 16.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed-9461295;  
RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
Thorepe A.;  
RT Isolation and identification of multiple neuropeptides of the  
RT allatostatin superfamily in the shore crab Carcinus maenas.";  
RT Eur. J. Biochem. 250:727-734(1997).

CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 RT allatostatin superfamily in the shore crab Carcinus maenas. \*;  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD.RES 8  
 SQ SEQUENCE 8 AA; 813 MW; 7C286545AB476678 CRC64;

Query Match 36.4%; Score 4; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 |  
 Db 8 L 8

RESULT 6  
 ID ALL7\_CARMA STANDARD; PRT; 8 AA.  
 AC P81820;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE CARCINUSSTATIN 17.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 OC NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=96121193; PubMed=9461295;  
 RA Duvé H., Johnson A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 "Isolation and identification of multiple neuropeptides of the  
 allatostatin superfamily in the shore crab Carcinus maenas. \*;  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD.RES 8  
 SQ SEQUENCE 8 AA; 858 MW; C82879D5AB46D865 CRC64;

Query Match 36.4%; Score 4; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 |  
 Db 8 L 8

RESULT 7  
 ID ALL8\_CARMA STANDARD; PRT; 8 AA.  
 AC P81821;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE CARCINUSSTATIN 18.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 OC NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duvé H., Johnson A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 Thorepe A.;

RT "Isolation and identification of multiple neuropeptides of the  
 allatostatin superfamily in the shore crab Carcinus maenas. \*;  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD.RES 8  
 SQ SEQUENCE 8 AA; 919 MW; C82879D5AB569AB5 CRC64;

Query Match 36.4%; Score 4; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 |  
 Db 8 L 8

RESULT 8  
 ID ALL1\_CYDPO STANDARD; PRT; 8 AA.  
 AC P82152;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE CYDIASTATIN 1.  
 OS Cydia pomonella (Codling moth).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.  
 OC NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Duvé H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 Davey M., East P.D., Thorepe A.;  
 "Lepidopteran peptides of the allatostatin superfamily. \*;  
 RL Peptides 18:1301-1309(1997).  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD.RES 8  
 SQ SEQUENCE 8 AA; 934 MW; C82879C45B51F775 CRC64;

Query Match 36.4%; Score 4; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 |  
 Db 8 L 8

RESULT 9  
 ID ALL3\_CYDPO STANDARD; PRT; 8 AA.  
 AC P82154;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE CYDIASTATIN 3.  
 OS Cydia pomonella (Codling moth).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.  
 OC NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Duvé H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,



RA Davey M., East P.D., Thorpe A.;  
 RT "Lepidopteran peptides of the allatostatin superfamily."  
 RL Peptides 18:1301-1309(1997).  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 8  
 SO SEQUENCE 8 AA; 926 MW; C82879D5AB477415 CRC64;

Query Match 36.4%; Score 4; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
 Db 8 L 8

RESULT 10  
 ALL6\_CALVO STANDARD; PRT; 8 AA.  
 AC P41840;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE CALLATOSTATIN 4 (LEU-CALLATOSTATIN 4).  
 OS Calliphora vomitoria (blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Streptoidea; Calliphoridae; Calliphora.  
 OX NCBI\_TaxID-27454;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-Phoracic ganglion;  
 RX MEDLINE-93211980; PubMed-8460157;  
 RA Dave H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,  
 Thorpe A.;  
 RT "Callatostatins: neuropeptides from the blowfly Calliphora vomitoria  
 with sequence homology to cockroach allatostatins.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).  
 RN [2]  
 RP CHARACTERIZATION.  
 RX MEDLINE-94291167; PubMed-8020069;  
 RA Dave H., Thorpe A.;  
 RT "Distribution and functional significance of leu-callatostatins in  
 the blowfly Calliphora vomitoria.";  
 RL Cell Tissue Res. 276:367-379(1994).  
 CC -1- FUNCTION: MAY ACT AS A NEUROTROPHIC FACTOR OR NEUROMODULATOR AND PLAY  
 A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE  
 INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO  
 BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO  
 FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.  
 CC -1- TISSUE SPECIFICITY: BRAIN, SUBESOPHAGEAL GANGLION, RETROCEPHAL  
 COMPLEX, THORACICO-ABDOMINAL GANGLION, PERIPHERAL NEUROSECRETORY  
 SYSTEM AND INTESTINE.  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 CC PIR: D47393; D47393.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 8  
 SO SEQUENCE 8 AA; 954 MW; D32879D5AB47740A CRC64;

Query Match 36.4%; Score 4; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
 Db 8 L 8

RESULT 11

ALL4\_CYPDPO STANDARD; PRT; 8 AA.  
 AC P82155;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE CYDIASTATIN 4.  
 OS Cydia pomonella (Coddling moth).  
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 CC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 OX NCBI\_TaxID-82600;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-Larva;  
 RX MEDLINE-98054539; PubMed-9392829;  
 RA Dave H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 Davey M., East P.D., Thorpe A.;  
 RT "Lepidopteran peptides of the allatostatin superfamily."  
 RL Peptides 18:1301-1309(1997).  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 8  
 SO SEQUENCE 8 AA; 910 MW; 922879D5AB47740D CRC64;

Query Match 36.4%; Score 4; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
 Db 8 L 8

RESULT 12  
 ALL5\_CYPDPO STANDARD; PRT; 8 AA.  
 AC P82156;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE CYDIASTATIN 5.  
 OS Cydia pomonella (Coddling moth).  
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 CC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 OX NCBI\_TaxID-82600;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-Larva;  
 RX MEDLINE-98054539; PubMed-9392829;  
 RA Dave H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 Davey M., East P.D., Thorpe A.;  
 RT "Lepidopteran peptides of the allatostatin superfamily."  
 RL Peptides 18:1301-1309(1997).  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 8  
 SO SEQUENCE 8 AA; 898 MW; 922879D5AB58640D CRC64;

Query Match 36.4%; Score 4; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
 Db 8 L 8

RESULT 13  
 ALL6\_CYPDPO

ID ALL6-CYDPO STANDARD; PRT; 8 AA.  
 AC P82157;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE CYDASTATIN 6.  
 OS Cydia pomonella (Codling moth).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 OX NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-LARVA;  
 RC MEDLINE=98054539; PubMed=9392829;  
 RA Duvé H., Johnsen A.H., Maestri J.-L., Scott A.G., Winstanley D.,  
 RA Duvé H., East F.D., Thorpe A.,  
 RT Peptide sequences of the allatostatin superfamily.\*;  
 RL Peptides 18:1301-1309(1997).  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD.RES 8 AA; 936 MW; 0B2879C45B573767 CRC64;  
 SQ SEQUENCE

Query Match 36.4%; Score 4; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
 Db 1 L 1

RESULT 14  
 ID ALL7-CARMA STANDARD; PRT; 8 AA.  
 AC P81809; P81810; P81804;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE CARCINUSTATIN 7 (COMMON: CARCINUSTATIN 6; CARCINUSTATIN 1).  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 CC Eudrachyura; Portunoidae; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-Cerebral ganglion, and Thoracic ganglion;  
 RC MEDLINE=98121193; PubMed=9461295;  
 RA Duvé H., Johnsen A.H., Maestri J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas.\*;  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT CHAIN 1 8 CARCINUSTATIN 7.  
 FT CHAIN 2 8 CARCINUSTATIN 6.  
 FT CHAIN 4 8 CARCINUSTATIN 1.  
 FT MOD.RES 8 AA; 825 MW; 922879CDB4775BD CRC64;  
 SQ SEQUENCE

Query Match 36.4%; Score 4; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
 Db 8 L 8

RESULT 15  
 ID ALL8-CARMA STANDARD; PRT; 8 AA.  
 AC P81811;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE CARCINUSTATIN 8.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eudrachyura; Portunoidae; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-Cerebral ganglion, and Thoracic ganglion;  
 RC MEDLINE=98121193; PubMed=9461295;  
 RA Duvé H., Johnsen A.H., Maestri J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas.\*;  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD.RES 8 AA; 795 MW; 922879CDB47687D CRC64;  
 SQ SEQUENCE

Query Match 36.4%; Score 4; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
 Db 8 L 8

Search completed: December 13, 2001, 12:01:34  
 Job time: 297 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 13, 2001, 12:01:16 : Search time 34.38 Seconds  
(without alignments)  
34.037 Million cell updates/sec

Title: US-09-424-080a-2  
Perfect score: 1 Lxxxxxxx 8  
Sequence: 1 Lxxxxxxx 8

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 287

Minimum DB seq length: 8  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP-archaea:\*  
2: SP-bacteria:\*  
3: SP-fungi:\*  
4: SP-human:\*  
5: SP-invertebrate:\*  
6: SP-mammal:\*  
7: SP-mmc:\*  
8: SP-organalle:\*  
9: SP-phage:\*  
10: SP-plant:\*  
11: SP-todent:\*  
12: SP-virus:\*  
13: SP-vertebrate:\*  
14: SP-unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	36.4	8	056429	thermus aqu
2	4	36.4	8	P72279	rhodococcus
3	4	36.4	8	045889	clostridium
4	4	36.4	8	085406	coxiella bu
5	4	36.4	8	087471	haemophilus
6	4	36.4	8	P77556	eschericchia
7	4	36.4	8	P77556	eschericchia
8	4	36.4	8	021594	neisseria m
9	4	36.4	8	021594	neisseria m
10	4	36.4	8	021594	neisseria m
11	4	36.4	8	021594	neisseria m
12	4	36.4	8	021594	neisseria m
13	4	36.4	8	021594	neisseria m
14	4	36.4	8	021594	neisseria m
15	4	36.4	8	021594	neisseria m
16	4	36.4	8	021594	neisseria m
17	4	36.4	8	021594	neisseria m
18	4	36.4	8	021594	neisseria m
19	4	36.4	8	021594	neisseria m

20	4	36.4	8	P82858	puccinia re
21	4	36.4	8	09HDS4	aspergillus
22	4	36.4	8	015889	homo sapien
23	4	36.4	8	015893	homo sapien
24	4	36.4	8	015894	homo sapien
25	4	36.4	8	015895	homo sapien
26	4	36.4	8	015901	homo sapien
27	4	36.4	8	016468	homo sapien
28	4	36.4	8	017404	homo sapien
29	4	36.4	8	017404	homo sapien
30	4	36.4	8	060773	homo sapien
31	4	36.4	8	09UMK7	homo sapien
32	4	36.4	8	09UMK7	homo sapien
33	4	36.4	8	09UMK7	homo sapien
34	4	36.4	8	09UMK7	homo sapien
35	4	36.4	8	09UMK7	homo sapien
36	4	36.4	8	09UMK7	homo sapien
37	4	36.4	8	09UMK7	homo sapien
38	4	36.4	8	09UMK7	homo sapien
39	4	36.4	8	09UMK7	homo sapien
40	4	36.4	8	09UMK7	homo sapien
41	4	36.4	8	09UMK7	homo sapien
42	4	36.4	8	09UMK7	homo sapien
43	4	36.4	8	09UMK7	homo sapien
44	4	36.4	8	09UMK7	homo sapien
45	4	36.4	8	09UMK7	homo sapien

## ALIGNMENTS

RESULT 1  
ID 056429 PRELIMINARY: PRT: 8 AA.  
AC 056429;  
DT 01-NOV-1996 (TREMELREL. 01, Created)  
DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)  
DT 01-NOV-1998 (TREMELREL. 08, Last annotation update)  
DE GAPDH (FRAGMENT).  
OS Thermus aquaticus (subsp. thermophilus).  
OC Bacteria; Thermus/Delinooccus group; Thermus group; Thermus.  
NCBI\_TaxID:274;  
RX MEDLINE:89025722; PubMed:3052437;  
RC SRAJIN-HB-8;  
RA Boven D., Littlechild J.A., Folchert J.L., Watson H.C., Hall L.;  
RT "Nucleotide sequence of the phosphoglycerate kinase gene from the  
RT extreme thermophile Thermus thermophilus. Comparison of the deduced  
RT amino acid sequence with that of the mesophilic yeast phosphoglycerate  
RT kinase." J. 254:509-517(1988).  
RL Biochem. J. 254:509-517(1988).  
DR EMBL: X12464; CAAS1005.1; -;  
FT NON\_TER 1  
SQ SEQUENCE 8 AA: 885 MW: 33C87333732C72B CRC64:

Query Match 36.4%; Score 4; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 L 1  
DB 2 L 2  
RESULT 2  
ID P72279 PRELIMINARY: PRT: 8 AA.  
AC P72279;  
DT 01-FEB-1997 (TREMELREL. 02, Created)  
DT 01-FEB-1997 (TREMELREL. 02, Last sequence update)  
DT 01-NOV-1998 (TREMELREL. 08, Last annotation update)

DE BIPIHENYL DIOXYGENASE (FRAGMENT).  
 GN BPHB.  
 OS Rhodococcus globerulus.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.  
 OK NCBI\_TaxID=33008;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95255652; PubMed=737502;  
 RA Asturias J.A., Diaz E., Timmis K.N.;  
 RT "The evolutionary relationship of biphenyl dioxygenase from gram-  
 positive Rhodococcus globerulus P6 to multicomponent dioxygenases from  
 gram-negative bacteria.";  
 RL Gene 158:111-18(1995).  
 DR EMBL; X80041; CAA56350.1; -  
 KW Dioxygenase.  
 FT NON\_TER  
 SQ SEQUENCE 8 AA; 989 MW; EMD2CBIAB6D73406 CRC64;

Query Match 36.4%; Score 4; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
 DB 3 L 3

RESULT 3  
 ID 045889 PRELIMINARY; PRT; 8 AA.  
 AC 045889;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)  
 DE HA-11 PROTEIN (FRAGMENT).  
 GN HA-11.  
 OS Clostridium botulinum.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;  
 OC Clostridium.  
 OK NCBI\_TaxID=1491;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=667AB;  
 RX MEDLINE=96210012; PubMed=8631890;  
 RA Hutson R.A., Zhou Y., Collins M.D., Johnson E.A., Hatheway C.L.,  
 RA Sugiyama H.;  
 RT "Genetic characterization of Clostridium botulinum type A containing  
 RT silent type B neurotoxin gene sequences.";  
 RL J. Biol. Chem. 271:10786-10792(1996).  
 DR EMBL; X87850; CAA61130.1; -  
 FT NON\_TER  
 SQ SEQUENCE 8 AA; 982 MW; FE29DIB40B02D5B6 CRC64;

Query Match 36.4%; Score 4; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
 DB 8 L 8

RESULT 4  
 ID 085406 PRELIMINARY; PRT; 8 AA.  
 AC 085406;  
 DT 01-NOV-1998 (TREMblrel. 08, Created)  
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)  
 DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)  
 DE HYPOTHETICAL 1.0 KDA PROTEIN (FRAGMENT).

OS Coxiella burnetii.  
 OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;  
 OC Coxiella group; Coxiella.  
 OK NCBI\_TaxID=777;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NINE MILE PHASE I;  
 RA Williams H., Jaeger C., Baljer G.;  
 RT "Physical and genetic map of the obligate intracellular bacterium  
 RT Coxiella burnetii.";  
 RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF064963; AA009947.1; -  
 KW Hypothetical protein.  
 FT NON\_TER  
 SQ SEQUENCE 8 AA; 993 MW; 046B5AA45372727 CRC64;

Query Match 36.4%; Score 4; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
 DB 1 L 1

RESULT 5  
 ID 087471 PRELIMINARY; PRT; 8 AA.  
 AC 087471;  
 DT 01-NOV-1998 (TREMblrel. 08, Created)  
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)  
 DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)  
 DE H1FA (FRAGMENT).  
 GN H1FA.  
 OS Haemophilus influenzae.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
 OC Haemophilus.  
 OK NCBI\_TaxID=727;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=EAGAN (E1A);  
 RX MEDLINE=98389689; PubMed=9721313;  
 RA Mlangi-Mutangadura T., Morlin G., Smith A.L., Eisenstark A.,  
 RA Golomb M.;  
 RT "Evolution of the major pilus gene cluster of Haemophilus  
 RT influenzae.";  
 RL J. Bacteriol. 180:4693-4703(1998).  
 DR EMBL; AF071762; AAC35830.1; -  
 FT NON\_TER  
 SQ SEQUENCE 8 AA; 876 MW; DAB44451A7272325 CRC64;

Query Match 36.4%; Score 4; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
 DB 3 L 3

RESULT 6  
 ID P77556 PRELIMINARY; PRT; 8 AA.  
 AC P77556;  
 DT 01-FEB-1997 (TREMblrel. 02, Created)  
 DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)  
 DT 01-JAN-1999 (TREMblrel. 09, Last annotation update)  
 DE TRAY (FRAGMENT).  
 GN Escherichia coli.  
 OC Plasmid IncFII R1.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 ON NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ECOR11;  
 RA MEDLINE-96400908; PubMed-8807284;  
 RT Boyd E.F., Hill C.W., Rich S.M., Hartl D.L.;  
 "Mosaic structure of plasmids from natural populations of Escherichia coli"; Genetics 143:1091-1100(1996).  
 RU Genetic; 143:1091-1100(1996).  
 DR EMBL; U50651; AAC44245.1;  
 DR EMBL; U50650; AAC44234.1;  
 DR EMBL; U50651; AAC44235.1;  
 DR EMBL; U50651; AAC44236.1;  
 DR EMBL; U50653; AAC44237.1;  
 DR EMBL; U50654; AAC44238.1;  
 DR EMBL; U50655; AAC44239.1;  
 DR EMBL; U50656; AAC44240.1;  
 DR EMBL; U50657; AAC44241.1;  
 DR EMBL; U50658; AAC44242.1;  
 DR EMBL; U50659; AAC44243.1;  
 DR EMBL; U50660; AAC44244.1;  
 RW Plasmid.  
 FT NON-TER  
 SO SEQUENCE 8 AA; 834 MW; D335A5B0544735A1 CRC64;

Query Match 36.4%; Score 4; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
 DB 3 L 3

RESULT 7  
 OS1594 PRELIMINARY; PRT; 8 AA.  
 AC OS1594;  
 DT 01-NOV-1996 (TREMUREL. 01, Created)  
 DT 01-NOV-1996 (TREMUREL. 01, Last sequence update)  
 DT 01-MAY-1999 (TREMUREL. 10, Last annotation update)  
 DE COBP PROTEIN (FRAGMENT).  
 OS Escherichia coli.  
 OC Plasmid Incpi ColV2-K94.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-86223772; PubMed-2423502;  
 RW Weber P.C., Palchaudhuri S.;  
 "Incompatibility repressor in a RepA-like replicon of the Incpi Plasmid ColV2-K94."; J. Bacteriol. 166:1106-1112(1986).  
 RT Plasmid ColV2-K94.  
 RL EMBL; M13472; AAA23194.1;  
 RW Plasmid.  
 FT NON-TER  
 SO SEQUENCE 8 AA; 998 MW; 0F37205AA73416D7 CRC64;

Query Match 36.4%; Score 4; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
 DB 1 L 1

RESULT 8

O9ZIE9  
 ID O9ZIE9 PRELIMINARY; PRT; 8 AA.  
 AC O9ZIE9;  
 DT 01-MAY-1999 (TREMUREL. 10, Created)  
 DT 01-MAY-1999 (TREMUREL. 10, Last sequence update)  
 DT 01-MAY-1999 (TREMUREL. 10, Last annotation update)  
 DE CARBAMOYL-PHOSPHATE SYNTHASE SUBUNIT B (FRAGMENT).  
 GN CARB.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-1527;  
 RX MEDLINE-95291461; PubMed-7773412;  
 RA Lawson F.S., Billowes F.M., Dillon J.A.;  
 "Organization of carbamoyl-phosphate synthase genes in Neisseria gonorrhoeae includes a large, variable intergenic sequence which is also present in other Neisseria species."; Microbiology 141:0-0(0).  
 RL Microbiology 141:0-0(0).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC Binkman P.S.L., Francis F.M., Dillon J.R.;  
 "Complexity of the variable sequence between the carbamoyl-phosphate synthase genes of Neisseria species."; RT Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AF029361; AAC78449.1;  
 DR EMBL; AF029361; AAC78449.1;  
 FT NON-TER  
 SO SEQUENCE 8 AA; 988 MW; FA372AB1B4032766 CRC64;

Query Match 36.4%; Score 4; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
 DB 7 L 7

RESULT 9  
 O9ZEZ9 PRELIMINARY; PRT; 8 AA.  
 ID O9ZEZ9;  
 AC O9ZEZ9;  
 DT 01-MAY-1999 (TREMUREL. 10, Created)  
 DT 01-MAY-1999 (TREMUREL. 10, Last sequence update)  
 DT 01-MAY-1999 (TREMUREL. 10, Last annotation update)  
 DE 2-ISOPROPYLMALATE SYNTHASE (EC 4.1.3.12) (FRAGMENT).  
 GN LEBU.  
 OS Buchnera aphidicola.  
 OG Plasmid pBrc1.  
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.  
 OX NCBI\_TaxID=9;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-99028904; PubMed-9812361;  
 RW Silva F.J., Van Ham R.C.H.J., Sabater B., Latorre A.;  
 "Structure and evolution of the leucine plasmids carried by the endosymbiont (Buchnera aphidicola) from aphids of the family Aphididae."; J. Eukaryot. Microbiol. Lett. 16:8:43-49(1998).  
 RT Aphididae.  
 RL EMBL; AJ006874; CAA07290.1;  
 RW Lyase; Plasmid.  
 FT NON-TER  
 SO SEQUENCE 8 AA; 917 MW; FE205042D6C5B446 CRC64;

Query Match 36.4%; Score 4; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1

Db 8 L 8

RESULT 10

ID Q9X3K1 PRELIMINARY; PRT; 8 AA.

AC Q9X3K1;

DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DE 01-NOV-1999 (TREMBLrel. 12, Last annotation update)

DE CYCROCHROME B (FRAGMENT).

GN PEBB.

OS Prochlorococcus sp.

OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;

NCBI\_TaxID=1220;

RM [1]

RP SEQUENCE FROM N.A.

RA Urbach E., Chisholm S.W.;

RT "Genetic diversity in Prochlorococcus populations flow cytometrically

sorted from the Sargasso Sea and Gulf Stream."

RL Ilanot. Oceanogr. 43:1615-1630(1998).

DR EMBL; AF070193; AAD23233.1; -

FT NON\_TER

SQ SEQUENCE 8 AA; 799 MW; 10376865B72866D3 CRC64;

OY 1 L 1

Db 4 L 4

RESULT 11

ID Q9RO57 PRELIMINARY; PRT; 8 AA.

AC Q9RO57;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE NIFS PROTEIN HOMOLOG (FRAGMENT).

GN NIFS.

OS Buchnera aphidicola.

OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.

NCBI\_TaxID=9;

RM [1]

RP SEQUENCE FROM N.A.

RA MEDLINE-20022990; PubMed-10555290;

RA Clark M.A., Moran N.A., Baumann P.;

RT "Sequence evolution in bacterial endosymbionts having extreme base

compositions."

RL Mol. Biol. Evol. 16:1586-1598(1999).

DR EMBL; AF130812; AAF13797.1; -

FT NON\_TER

SQ SEQUENCE 8 AA; 980 MW; F3A73B504771A336 CRC64;

OY 1 L 1

Db 7 L 7

RESULT 12

ID Q9RO49 PRELIMINARY; PRT; 8 AA.

AC Q9RO49;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE 31,000 DA PRODUCT OF ORFB.

FT NON\_TER

SQ SEQUENCE 8 AA; 992 MW; F3A73B5047672336 CRC64;

OY 1 L 1

Db 4 L 4

RESULT 14

ID Q9R5R2 PRELIMINARY; PRT; 8 AA.

AC Q9R5R2;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

FT NON\_TER

SQ SEQUENCE 8 AA; 985 MW; E8B41B1A735B446 CRC64;

OY 1 L 1

Db 4 L 4

RESULT 13

ID Q9R9C2 PRELIMINARY; PRT; 8 AA.

AC Q9R9C2;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE Borrelia burgdorferi (Lyme disease spirochete).

OS Plasmid cp32-3.

OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.

NCBI\_TaxID=139;

RM [1]

RP SEQUENCE FROM N.A.

RA STRAIN-B31;

RA MEDLINE-98361033; PubMed-9695920;

RA Stevenson B., Casjens S., Rosa P.;

RT "Evidence of past recombination events among the genes encoding the

Erp antigens of Borrelia burgdorferi."

RL Microbiology 144:0-0(0).

DR EMBL; AF022480; AAC35445.1; -

FT NON\_TER

SQ SEQUENCE 8 AA; 985 MW; E8B41B1A735B446 CRC64;

OY 1 L 1

Db 3 L 3

RESULT 13

ID Q9R9C2 PRELIMINARY; PRT; 8 AA.

AC Q9R9C2;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE PLASMID CP32-3, POSSIBLE PARTITION PROTEIN, COMPLETE CDS (FRAGMENT).

OS Borrelia burgdorferi (Lyme disease spirochete).

OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.

NCBI\_TaxID=139;

RM [1]

RP SEQUENCE FROM N.A.

RA STRAIN-B31;

RA MEDLINE-98361033; PubMed-9695920;

RA Stevenson B., Casjens S., Rosa P.;

RT "Evidence of past recombination events among the genes encoding the

Erp antigens of Borrelia burgdorferi."

RL Microbiology 144:0-0(0).

DR EMBL; AF022480; AAC35445.1; -

FT NON\_TER

SQ SEQUENCE 8 AA; 985 MW; E8B41B1A735B446 CRC64;

OY 1 L 1

Db 3 L 3

RESULT 13

ID Q9R9C2 PRELIMINARY; PRT; 8 AA.

AC Q9R9C2;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE PLASMID CP32-3, POSSIBLE PARTITION PROTEIN, COMPLETE CDS (FRAGMENT).

OS Borrelia burgdorferi (Lyme disease spirochete).

OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.

NCBI\_TaxID=139;

RM [1]

RP SEQUENCE FROM N.A.

RA STRAIN-B31;

RA MEDLINE-98361033; PubMed-9695920;

RA Stevenson B., Casjens S., Rosa P.;

RT "Evidence of past recombination events among the genes encoding the

Erp antigens of Borrelia burgdorferi."

RL Microbiology 144:0-0(0).

DR EMBL; AF022480; AAC35445.1; -

FT NON\_TER

SQ SEQUENCE 8 AA; 985 MW; E8B41B1A735B446 CRC64;

OY 1 L 1

Db 3 L 3

RESULT 13

ID Q9R9C2 PRELIMINARY; PRT; 8 AA.

AC Q9R9C2;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE PLASMID CP32-3, POSSIBLE PARTITION PROTEIN, COMPLETE CDS (FRAGMENT).

OS Borrelia burgdorferi (Lyme disease spirochete).

OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.

NCBI\_TaxID=139;

RM [1]

RP SEQUENCE FROM N.A.

RA STRAIN-B31;

RA MEDLINE-98361033; PubMed-9695920;

RA Stevenson B., Casjens S., Rosa P.;

RT "Evidence of past recombination events among the genes encoding the

Erp antigens of Borrelia burgdorferi."

RL Microbiology 144:0-0(0).

DR EMBL; AF022480; AAC35445.1; -

FT NON\_TER

SQ SEQUENCE 8 AA; 985 MW; E8B41B1A735B446 CRC64;

OY 1 L 1

Db 3 L 3

RESULT 13

ID Q9R9C2 PRELIMINARY; PRT; 8 AA.

AC Q9R9C2;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE PLASMID CP32-3, POSSIBLE PARTITION PROTEIN, COMPLETE CDS (FRAGMENT).

OS Borrelia burgdorferi (Lyme disease spirochete).

OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.

NCBI\_TaxID=139;

RM [1]

RP SEQUENCE FROM N.A.

RA STRAIN-B31;

RA MEDLINE-98361033; PubMed-9695920;

RA Stevenson B., Casjens S., Rosa P.;

RT "Evidence of past recombination events among the genes encoding the

Erp antigens of Borrelia burgdorferi."

RL Microbiology 144:0-0(0).

DR EMBL; AF022480; AAC35445.1; -

FT NON\_TER

SQ SEQUENCE 8 AA; 985 MW; E8B41B1A735B446 CRC64;

OY 1 L 1

Db 3 L 3

RESULT 13

ID Q9R9C2 PRELIMINARY; PRT; 8 AA.

AC Q9R9C2;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE PLASMID CP32-3, POSSIBLE PARTITION PROTEIN, COMPLETE CDS (FRAGMENT).

OS Borrelia burgdorferi (Lyme disease spirochete).

OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.

NCBI\_TaxID=139;

RM [1]

RP SEQUENCE FROM N.A.

RA STRAIN-B31;

RA MEDLINE-98361033; PubMed-9695920;

RA Stevenson B., Casjens S., Rosa P.;

RT "Evidence of past recombination events among the genes encoding the

Erp antigens of Borrelia burgdorferi."

RL Microbiology 144:0-0(0).

DR EMBL; AF022480; AAC35445.1; -

FT NON\_TER

SQ SEQUENCE 8 AA; 985 MW; E8B41B1A735B446 CRC64;

OY 1 L 1

Db 3 L 3

RESULT 13

ID Q9R9C2 PRELIMINARY; PRT; 8 AA.

AC Q9R9C2;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE PLASMID CP32-3, POSSIBLE PARTITION PROTEIN, COMPLETE CDS (FRAGMENT).

OS Borrelia burgdorferi (Lyme disease spirochete).

OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.

NCBI\_TaxID=139;

RM [1]

RP SEQUENCE FROM N.A.

RA STRAIN-B31;

RA MEDLINE-98361033; PubMed-9695920;

RA Stevenson B., Casjens S., Rosa P.;

RT "Evidence of past recombination events among the genes encoding the

Erp antigens of Borrelia burgdorferi."

RL Microbiology 144:0-0(0).

DR EMBL; AF022480; AAC35445.1; -

FT NON\_TER

SQ SEQUENCE 8 AA; 985 MW; E8B41B1A735B446 CRC64;

OY 1 L 1

Db 3 L 3

RESULT 13

ID Q9R9C2 PRELIMINARY; PRT; 8 AA.

AC Q9R9C2;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE PLASMID CP32-3, POSSIBLE PARTITION PROTEIN, COMPLETE CDS (FRAGMENT).

OS Borrelia burgdorferi (Lyme disease spirochete).

OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.

NCBI\_TaxID=139;

RM [1]

RP SEQUENCE FROM N.A.

RA STRAIN-B31;

RA MEDLINE-98361033; PubMed-9695920;

RA Stevenson B., Casjens S., Rosa P.;

RT "Evidence of past recombination events among the genes encoding the

Erp antigens of Borrelia burgdorferi."

RL Microbiology 144:0-0(0).

DR EMBL; AF022480; AAC35445.1; -

FT NON\_TER

SQ SEQUENCE 8 AA; 985 MW; E8B41B1A735B446 CRC64;

OY 1 L 1

Db 3 L 3

RESULT 13

ID Q9R9C2 PRELIMINARY; PRT; 8 AA.

AC Q9R9C2;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

OS Shigella dysenteriae.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Shigella.  
 OX NCBI\_TaxID-622;  
 RN [1]  
 RP MEDLINE-92085268; PubMed-1660923;  
 RA Polard P., Prere M.F., Chandler M., Fayet O.;  
 RT "Programmed translational frameshifting and initiation at an Auu codon  
 in gene expression of bacterial insertion sequence IS911.";  
 RL J. Mol. Biol. 222:465-477(1991).  
 SQ SEQUENCE 8 AA; 902 MW; FE2DCAFB586AE336 CRC64;

Query Match 36.4%; Score 4; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
 DB 8 L 8

RESULT 15  
 O9R4M3  
 ID O9R4M3 PRELIMINARY; PRT; 8 AA.  
 AC O9R4M3;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE COB1-BACTERIAL SEX PHEROMONE.  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;  
 OC Enterococcus.  
 OX NCBI\_TaxID-1351;  
 RN [1]  
 RP MEDLINE-95290767; PubMed-7772836;  
 RA Nakayama J., Abe Y., Ono Y., Isogai A., Suzuki A.;  
 RT "Isolation and structure of the Enterococcus faecalis sex pheromone,  
 COB1, that induces conjugal transfer of the hemolysin/bacteriocin  
 plasmids, pOB1 and pT11.";  
 RL Biosci. Biotechnol. Biochem. 59:703-705(1995).  
 SQ SEQUENCE 8 AA; 741 MW; 83D8732C732CDC2 CRC64;

Query Match 36.4%; Score 4; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
 DB 4 L 4

Search completed: December 13, 2001, 12:01:16  
 Job time: 304 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 13, 2001, 11:57:18 ; Search time 36.87 Seconds  
(without alignments)  
16.072 Million cell updates/sec

Title: US-09-424-080A-2  
Sequence: 1 LXXXXXX 8

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 15187

Minimum DB seq length: 8  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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2: /SID88/gcgdata/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/AA1984.DAT.*
6: /SID88/gcgdata/geneseq/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/AA1986.DAT.*
8: /SID88/gcgdata/geneseq/AA1987.DAT.*
9: /SID88/gcgdata/geneseq/AA1988.DAT.*
10: /SID88/gcgdata/geneseq/AA1989.DAT.*
11: /SID88/gcgdata/geneseq/AA1990.DAT.*
12: /SID88/gcgdata/geneseq/AA1991.DAT.*
13: /SID88/gcgdata/geneseq/AA1992.DAT.*
14: /SID88/gcgdata/geneseq/AA1993.DAT.*
15: /SID88/gcgdata/geneseq/AA1994.DAT.*
16: /SID88/gcgdata/geneseq/AA1995.DAT.*
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19: /SID88/gcgdata/geneseq/AA1998.DAT.*
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22: /SID88/gcgdata/geneseq/AA2001.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	36.4	8	AA10369	Peptide secretin d
2	4	36.4	8	AA10585	GH, gastric and p
3	4	36.4	8	AA10461	Antibiotic octapep
4	4	36.4	8	AA10462	Antibiotic octapep
5	4	36.4	8	AA10463	Antibiotic octapep
6	4	36.4	8	AA10464	Antibiotic octapep
7	4	36.4	8	AA10291	Bombesin analog pe
8	4	36.4	8	AA10292	Bombesin analog pe
9	4	36.4	8	AA10293	Bombesin analog pe
10	4	36.4	8	AA10294	Bombesin analog pe
11	4	36.4	8	AA10295	Opitoid Peptide 2.

12	4	36.4	8	AA10374	Cargutocin, Synth
13	4	36.4	8	AA10381	Protected insulin
14	4	36.4	8	AA10382	Protected insulin
15	4	36.4	8	AA10383	Gastrointestinal m
16	4	36.4	8	AA10483	De-amino-6-carba-o
17	4	36.4	8	AA10485	Novel antibiotic n
18	4	36.4	8	AA10486	Novel antibiotic n
19	4	36.4	8	AA10487	Novel antibiotic n
20	4	36.4	8	AA10488	Novel antibiotic n
21	4	36.4	8	AA10489	Novel antibiotic n
22	4	36.4	8	AA10490	Novel antibiotic n
23	4	36.4	8	AA10491	Novel antibiotic n
24	4	36.4	8	AA10492	Novel antibiotic n
25	4	36.4	8	AA10493	Novel antibiotic n
26	4	36.4	8	AA10494	Novel antibiotic n
27	4	36.4	8	AA10495	Novel antibiotic n
28	4	36.4	8	AA10496	Novel antibiotic n
29	4	36.4	8	AA10497	Novel antibiotic n
30	4	36.4	8	AA10498	Novel antibiotic n
31	4	36.4	8	AA10499	Novel antibiotic n
32	4	36.4	8	AA10500	Novel antibiotic n
33	4	36.4	8	AA10501	Novel antibiotic n
34	4	36.4	8	AA10502	Novel antibiotic n
35	4	36.4	8	AA10503	Novel antibiotic n
36	4	36.4	8	AA10504	Novel antibiotic n
37	4	36.4	8	AA10505	Novel antibiotic n
38	4	36.4	8	AA10506	Novel antibiotic n
39	4	36.4	8	AA10507	Novel antibiotic n
40	4	36.4	8	AA10508	Novel antibiotic n
41	4	36.4	8	AA10509	Novel antibiotic n
42	4	36.4	8	AA10510	Novel antibiotic n
43	4	36.4	8	AA10511	Novel antibiotic n
44	4	36.4	8	AA10512	Novel antibiotic n
45	4	36.4	8	AA10513	Novel antibiotic n

#### ALIGNMENTS

RESULT 1	AA10369	standard; Protein; 8 AA.
ID	AA10369	
AC	AA10369	
DT	16-DEC-1992	(first entry)
XX	Peptide secretin derivative #8.	
DE	secretin; insulin; diabetes; pancreas; islets of langerhans; glucose.	
OS	Synthetic.	
XX		
EH	Key	Location/Qualifiers
FT	Modified site	/label= OTHER
FT		/note= "pyroglutamic acid"
FT	Misc-difference	/label= OTHER
FT		/note= "OR3 or -NR12
FT		where R1 and R2 are H, C1-C6 alkyl,
FT		C3-C8 cycloalkyl, R1 and R2 may also be
FT		linked together to form a cyclic gp having
FT		at least 1 hetero atom ie the amino bonded N,
FT		opt. confg. an additional hetero atom eg. N,
FT		O, or S.
FT		where R3 is H, C1-C6 alkyl, C3-C8 cycloalkyl,
FT		benzyl, phenacyl, phthalimidomethyl,
FT		beta-methylthioethyl, 4-picolyl, and benzyl
FT		substituted with nitro, methoxy, methyl,
FT		halogen."
PN	USA265884-A.	



XX 05-MAY-1981.  
 PD 24-SEP-1979; 79US-0078425.  
 XX  
 PF 05-SEP-1979; 79DK-0003710.  
 PR 28-SEP-1978; 78DK-0004304.  
 XX  
 PA (NORI ) NORDISK INSULINLAB.  
 XX  
 PI Kofod H;  
 DR WPI: 1981-38054D/21 (38054D);  
 XX  
 PR Secretin related poly:peptide(s) - which potentiate glucose  
 stimulated secretion of insulin  
 XX  
 PS Claim 2; Column 6; 4pp: English.  
 CC This peptide is a derivative of the intestinal hormone secretin.  
 CC They potentiate the glucose stimulated secretion of insulin from  
 CC Langerhans' islets. They may be used to treat diabetics who have  
 CC themselves lost the ability to liberate insulin from the Langerhans  
 CC islets.  
 CC  
 SQ Sequence 8 AA;

Query Match 36.4%; Score 4; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
 |  
 DB 5 1 5

RESULT 2  
 AAP10585  
 ID AAP10585 standard; Protein; 8 AA.  
 AC AAP10585;  
 XX  
 DT 23-DEC-1992 (first entry)  
 XX  
 DE GH, gastric and pancreatic secretion inhibitor (1).  
 XX  
 KW Growth hormone; diabetes; acromegaly.  
 XX  
 OS Synthetic.  
 XX  
 FT Key Location/Qualifiers  
 FT MISC-difference 1 /note= "D-form residue"  
 FT MISC-difference 4 /note= "D-form residue"  
 FT MISC-difference 8 /label= LEU, OTHER  
 FT /note= "LEU-OL"  
 FT Disulfide-bond 2..7  
 XX  
 PN EP29579-A.  
 XX  
 PD 03-JUN-1981.  
 XX  
 PE 13-JUN-1988; 88EP-0057316.  
 XX  
 PR 13-JUN-1980; 80CH-0004574.  
 PR 27-NOV-1979; 79CH-0010524.  
 XX  
 PA (SANO ) SANDOZ AG.  
 XX  
 PI Bauer W, Pless J;

XX WPI: 1981-42362D/24 (42362D).  
 DR Polypeptide(s) contg. cysteine-terminal hexa:peptide fragment -  
 PR useful as growth-hormone, gastric and pancreatic secretion  
 PT inhibitors  
 XX  
 PS Claim 4; Page 31; 35pp: English.  
 CC The peptide inhibits growth hormone secretion and can be used to  
 CC treat diabetes, angiopathy and acromegaly. It also inhibits gastric  
 CC and pancreatic secretion and can be used to treat gastrointestinal  
 CC disorders.  
 CC  
 SQ Sequence 8 AA;

Query Match 36.4%; Score 4; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
 |  
 DB 8 1 8

RESULT 3  
 AAP10461  
 ID AAP10461 standard; peptide; 8 AA.  
 AC AAP10461;  
 XX  
 DT 17-DEC-1992 (first entry)  
 XX  
 DE Antibiotic octapeptin 1.  
 XX  
 KW Staphylococcus aureus; Streptococcus pyogenes; Bacillus subtilis;  
 KW Salmonella typhimurium; Shigella sonnei Ohara.  
 XX  
 OS Synthetic.  
 XX  
 FT Key Location/Qualifiers  
 FT Modified-site 1 /note= "D-Ser acetylated with beta-hydroxy-  
 FT antelsoundecanoic acid; forms a peptide  
 FT bond with Leu at position 8"  
 FT Modified-site 2 /label= OTHER  
 FT /note= "alpha, gamma-diaminobutyric acid"  
 FT Modified-site 3 /label= OTHER  
 FT /note= "alpha, gamma-diaminobutyric acid"  
 FT Modified-site 6 /label= OTHER  
 FT /note= "alpha, gamma-diaminobutyric acid"  
 FT Modified-site 7 /label= OTHER  
 FT /note= "alpha, gamma-diaminobutyric acid"  
 FT MISC-difference 8 /note= "forms peptide bond with Dab at position 1"  
 FT  
 XX  
 PN JP56087596-A.  
 XX  
 PD 16-JUL-1981.  
 XX  
 PE 18-DEC-1979; 79JP-0165150.  
 XX  
 PR 18-DEC-1979; 79JP-0165150.  
 XX  
 PA (SHIO ) SHIONOGI KK.  
 XX  
 DR WPI: 1981-63474D/35 (63474D).

PT Antibiotic octapeptin D - prepd. by cultivating *Bacillus* gp. no.  
 JP-301  
 XX  
 PS Claim 2; Page 1; 6pp; Japanese.  
 CC The sequences given in AAP10461-4 are antibiotic octapeptins which  
 CC have antimicrobial activity. They are active against *Staphylococcus*  
 CC aureus FDA209P, *Streptococcus pyogenes* C-203, *Bacillus subtilis* PCI  
 CC 219, *Salmonella typhimurium* and *Shigella sonnei* Ohara.  
 CC  
 XX  
 SQ Sequence 8 AA;

Query Match 36.4%; Score 4; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 Db 4 1 4

## RESULT 4

AAP10462  
 ID AAP10462 standard; Protein; 8 AA.

AC AAP10462;

DT 17-DEC-1992 (first entry)

DE Antibiotic octapeptin 2.

XX *Staphylococcus aureus*; *Streptococcus pyogenes*; *Bacillus subtilis*;

KW *Salmonella typhimurium*; *Shigella sonnei* Ohara.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note- "D-Ser acetylated with beta-hydroxy-

FT Isodecanoic acid; forms a peptide

FT bond with Leu at position 8"

FT Modified-site 2 /label= OTHER

FT /note= "alpha, gamma-diaminobutyric acid"

FT Modified-site 3 /label= OTHER

FT /note= "alpha, gamma-diaminobutyric acid"

FT Modified-site 6 /label= OTHER

FT /note= "alpha, gamma-diaminobutyric acid"

FT Modified-site 7 /label= OTHER

FT /note= "alpha, gamma-diaminobutyric acid"

FT Modified-site 8 /label= OTHER

FT /note= "alpha, gamma-diaminobutyric acid"

FT MISC-difference 8 /note= "Forms peptide bond with Dab at position 1"

XX JP56087596-A.

XX 16-JUL-1981.

XX 18-DEC-1979; 79JP-0165150.

XX 18-DEC-1979; 79JP-0165150.

XX (SHIO) SHIONOGI KK.

XX WPI; 1981-63474D/35 (63474D).

XX Antibiotic octapeptin D - prepd. by cultivating *Bacillus* gp. no.

PT JP-301

XX Claim 3; Page 1; 6pp; Japanese.

XX The sequences given in AAP10461-4 are antibiotic octapeptins which  
 CC have antimicrobial activity. They are active against *Staphylococcus*  
 CC aureus FDA209P, *Streptococcus pyogenes* C-203, *Bacillus subtilis* PCI  
 CC 219, *Salmonella typhimurium* and *Shigella sonnei* Ohara.  
 CC  
 XX  
 SQ Sequence 8 AA;

Query Match 36.4%; Score 4; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
 Db 4 1 4

## RESULT 5

AAP10463  
 ID AAP10463 standard; Protein; 8 AA.

AC AAP10463;

DT 17-DEC-1992 (first entry)

DE Antibiotic octapeptin 3.

XX *Staphylococcus aureus*; *Streptococcus pyogenes*; *Bacillus subtilis*;

KW *Salmonella typhimurium*; *Shigella sonnei* Ohara.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note- "D-Ser acetylated with beta-hydroxy-

FT decanoic acid; forms a peptide

FT bond with Leu at position 8"

FT Modified-site 2 /label= OTHER

FT /note= "alpha, gamma-diaminobutyric acid"

FT Modified-site 3 /label= OTHER

FT /note= "alpha, gamma-diaminobutyric acid"

FT Modified-site 6 /label= OTHER

FT /note= "alpha, gamma-diaminobutyric acid"

FT Modified-site 7 /label= OTHER

FT /note= "alpha, gamma-diaminobutyric acid"

FT Modified-site 8 /note= "Forms peptide bond with Dab at position 1"

XX JP56087596-A.

XX 16-JUL-1981.

XX 18-DEC-1979; 79JP-0165150.

XX 18-DEC-1979; 79JP-0165150.

XX (SHIO) SHIONOGI KK.

XX WPI; 1981-63474D/35 (63474D).

XX Antibiotic octapeptin D - prepd. by cultivating *Bacillus* gp. no.

PT JP-301

XX Claim 4; Page 1; 6pp; Japanese.

XX The sequences given in AAP10461-4 are antibiotic octapeptins which

CC have antimicrobial activity. They are active against *Staphylococcus*

CC aureus FDA209P, *Streptococcus pyogenes* C-203, *Bacillus subtilis* PCI

CC



AC AAP20292;  
XX  
DT 09-DEC-1992 (first entry)  
XX  
DE Bombesin analog peptide.  
XX  
KW Bombesin; hypothemic; analgesic.  
XX  
OS Synthetic.  
PN US4331661-A.  
XX  
PD 25-MAY-1982.  
XX  
PF 03-OCT-1980; 80US-0193621.  
XX  
PK 03-OCT-1980; 80US-0193621.  
XX  
PA (SALK-) SALK INST BIOLOGICA.  
PI Markl WE, Brown MR, Rivier JEF;  
XX  
DR WPI; 1982-48049E/23 (48049E).  
XX  
PT Octa:peptide bombesin analogues - having hypothemic and  
XX  
PS analgesic props.  
PS Claim 4; Column 7; 5pp; English.  
XX  
CC The peptide may be preceded by a formyl, acetyl, propionyl, acrylyl  
CC or benzoyl group at its C-terminal. The peptide may be used for  
CC reducing the body temp. of a mammal, as well as for inducing  
CC analgesia. It produces hypothemia when injected i.c., but not  
CC when given i.v. or s.c. See also AAP20291, AAP20293-4.  
XX  
SQ Sequence 8 AA;  
  
Query Match 36.4%; Score 4; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 1 1  
DB 7 1 7  
  
RESULT 9  
AAP20293  
ID AAP20293 standard; peptide; 8 AA.  
XX  
AC AAP20293;  
XX  
DT 09-DEC-1992 (first entry)  
XX  
DE Bombesin analog peptide.  
XX  
KW Bombesin; hypothemic; analgesic.  
XX  
OS Synthetic.  
PN US4331661-A.  
XX  
PD 25-MAY-1982.  
XX  
PF 03-OCT-1980; 80US-0193621.  
XX  
PK 03-OCT-1980; 80US-0193621.  
XX

PA (SALK-) SALK INST BIOLOGICA.  
XX  
PI Markl WE, Brown MR, Rivier JEF;  
XX  
DR WPI; 1982-48049E/23 (48049E).  
XX  
PT Octa:peptide bombesin analogues - having hypothemic and  
XX  
PS analgesic props.  
PS Claim 6; Column 7; 5pp; English.  
XX  
CC The peptide may be preceded by a formyl, acetyl, propionyl, acrylyl  
CC or benzoyl group at its C-terminal. The peptide may be used for  
CC reducing the body temp. of a mammal, as well as for inducing  
CC analgesia. It produces hypothemia when injected i.c., but not  
CC when given i.v. or s.c. See also AAP20291-2, AAP20294.  
XX  
SQ Sequence 8 AA;  
  
Query Match 36.4%; Score 4; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 1 1  
DB 7 1 7  
  
RESULT 10  
AAP20294  
ID AAP20294 standard; peptide; 8 AA.  
XX  
AC AAP20294;  
XX  
DT 09-DEC-1992 (first entry)  
XX  
DE Bombesin analog peptide.  
XX  
KW Bombesin; hypothemic; analgesic.  
XX  
OS Synthetic.  
PN US4331661-A.  
XX  
PD 25-MAY-1982.  
XX  
PF 03-OCT-1980; 80US-0193621.  
XX  
PK 03-OCT-1980; 80US-0193621.  
XX  
PA (SALK-) SALK INST BIOLOGICA.  
PI Markl WE, Brown MR, Rivier JEF;  
XX  
DR WPI; 1982-48049E/23 (48049E).  
XX  
PT Octa:peptide bombesin analogues - having hypothemic and  
XX  
PS analgesic props.  
PS Claim 8; Column 8; 5pp; English.  
XX  
CC The peptide may be preceded by a formyl, acetyl, propionyl, acrylyl  
CC or benzoyl group at its C-terminal. The peptide may be used for  
CC reducing the body temp. of a mammal, as well as for inducing  
CC analgesia. It produces hypothemia when injected i.c., but not  
CC when given i.v. or s.c. See also AAP20291-3.

XX Sequence 8 AA;

Query Match 36.4%; Score 4; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
DB 7 1 7

## RESULT 11

AAP20254 ID AAP20254 standard; Protein; 8 AA.  
XX AAP20254;  
DT 27-NOV-1992 (first entry)  
XX  
DE Opioid peptide 2.  
XX  
KW Hypothalamus; acetic acid; chromatography.  
XX  
OS Sus scrofa.  
XX  
PN JP57134451-A.  
XX  
PD 19-AUG-1982.  
XX  
PF 13-FEB-1981; 81JP-0020707.  
XX  
PR 13-FEB-1981; 81JP-0020707.  
XX  
PA (SUNC) SUN CHEMICAL CORP.  
XX  
DK WPI: 1982-82141E/39 (82141E).  
XX  
FI Opiate peptide cpds. - useful as morphine-like analgesics  
XX  
PS Claim 1; Page 2; 6pp; Japanese.  
XX  
CC The sequences given in AAP20253-4 are opioid peptides. They can be  
CC used as morphine-like analgesics. They can be obtained by  
CC extraction of porcine hypothalamus with acetic acid, followed by  
CC chromatography with "Sephadex" and by HPLC with "Bondapak C-18".  
XX  
SQ Sequence 8 AA;

Query Match 36.4%; Score 4; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
DB 5 1 5

## RESULT 12

AAP20374 ID AAP20374 standard; Protein; 8 AA.  
XX AAP20374;  
DT 18-JAN-1993 (second entry)  
XX  
DE Cargotocin.  
XX  
KW Oxytocic agent; linear molecule; cyclization.  
XX  
OS Synthetic.

XX Key Location/Qualifiers  
FH Modified-site 5  
FT /label= OTHER  
FT /note= "L-aminosuberic acid"

FT Modified-site 1  
FT /note= "The amino gp of Tyr1 is condensed to the  
FT side chain of Asu5."  
FT Modified-site 5  
FT /note= "The amino gp of Tyr1 is condensed to the  
FT side chain of Asu5."

XX JP57062245-A.  
PN JP57062246-A.  
XX

XX 15-APR-1982.

XX 01-OCT-1980; 80JP-0137970.  
XX 01-OCT-1980; 80JP-0137970.

XX (YOSH) YOSHITOMI PHARM IND KK.  
XX WPI: 1982-42246E/21 (42246E).

XX Cargotocin prep. from L-amino suberic acid ester - by successive  
FT prolongation of peptide chain followed by its cyclization and  
FT reaction with hydrazine  
XX  
PS Disclosure: Page 1; 4pp; Japanese.

XX The sequence given is carginocin which is produced by reacting a  
CC precursor molecule (see also AAP20373) with a linear peptide  
CC H-Gly-Leu-Gly-NH2 to produce the product molecule. Carginocin is  
CC useful as an oxytocic agent. The product provides high solubility  
CC of reactants in solvents and high yield in cyclization.

XX SQ Sequence 8 AA;

Query Match 36.4%; Score 4; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
DB 7 1 7

## RESULT 13

AAP20141 ID AAP20141 standard; peptide; 8 AA.  
XX AAP20141;  
DT 27-NOV-1992 (first entry)  
XX  
DE Protected insulin B-chain (1).  
XX  
KW Hydrazide; DNP; 2,4-dinitrophenyl; DPM; diphenylmethyl.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT /note= "Alpha-protected, removable by mild acid  
FT hydrolysis"  
FT Modified-site 5  
FT /note= "DNP-protected or His-H"  
FT Duplication 7  
FT /note= "DPM-protected"  
FT Modified-site 8  
FT /note= "alkylated (sic) or amidated"

XX DD155321-A.  
 XX 02-JUN-1982.  
 XX 08-AUG-1980; 80DD-0223203.  
 XX 15-DEC-1980; 80DD-0226078.  
 XX (AROL/) AROLD H.  
 XX AROLD H, Mueller A, Schwuchow C;  
 XX WPI: 1982-83706E/40 (83706E).  
 XX Prepn. of protected insulin B-chain octa-peptide - using  
 XX di:nitro-phenyl gp. for histidine protection  
 XX Claim 1; Page 10; 11pp; German.  
 XX The cpd. is useful as intermediate for synthesis of insulin or its  
 XX B chain. The DNP gp. provides temporary protection for the His side  
 XX chain and is readily removed by hydrazinolysis, e.g. during  
 XX conversion of the cpd. to the hydrazide.  
 XX Sequence 8 AA;

Query Match 36.4%; Score 4; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 1 L 1  
 Db 6 1 6

## RESULT 14

AAP20381

ID AAP20381 standard; Protein; 8 AA.

XX AAP20381;

XX 27-NOV-1992 (first entry)

XX Protected insulin B-chain (2).

XX DNP; 2,4-dinitrophenyl; DPM; diphenylmethyl.

XX Synthetic.

XX Key Location/Qualifiers

XX Modified-site 1 /note="Boc-protected"

XX Modified-site 5 /note="DNP-protected"

XX Modified-site 7 /note="DPM-protected"

XX Modified-site 8 /note="Gly-OMe"

XX DD155321-A.

XX 02-JUN-1982.

XX 08-AUG-1980; 80DD-0223203.

XX 15-DEC-1980; 80DD-0226078.

XX (AROL/) AROLD H.

XX AROLD H, Mueller A, Schwuchow C;

DR WPI: 1982-83706E/40 (83706E).  
 XX Prepn. of protected insulin B-chain octa-peptide - using  
 XX di:nitro-phenyl gp. for histidine protection  
 XX Example 8; Page 8; 11pp; German.  
 XX The cpd. is useful as intermediate for synthesis of insulin or its  
 XX B chain.  
 XX Sequence 8 AA;

Query Match 36.4%; Score 4; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 L 1  
 Db 6 1 6

## RESULT 15

AAP20382

ID AAP20382 standard; Protein; 8 AA.

XX AAP20382;

XX 27-NOV-1992 (first entry)

XX Protected insulin B-chain (3).

XX DNP; 2,4-dinitrophenyl; DPM; diphenylmethyl.

XX Synthetic.

XX Key Location/Qualifiers

XX Modified-site 1 /note="Boc-protected"

XX Duplication 7 /note="DPM-protected"

XX Modified-site 8 /note="amidated"

XX DD155321-A.

XX 02-JUN-1982.

XX 08-AUG-1980; 80DD-0223203.

XX 15-DEC-1980; 80DD-0226078.

XX (AROL/) AROLD H.

XX AROLD H, Mueller A, Schwuchow C;

XX WPI: 1982-83706E/40 (83706E).

XX Prepn. of protected insulin B-chain octa-peptide - using  
 XX di:nitro-phenyl gp. for histidine protection

XX Example 9; Page 9; 11pp; German.

XX The cpd. is useful as intermediate for synthesis of insulin or its  
 XX B chain.

XX Sequence 8 AA;

Query Match 36.4%; Score 4; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Thu Dec 13 12:06:10 2001

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Page 8

OY 1 E 1  
Db 6 1 6

Search completed: December 13, 2001, 11:57:18  
Job time: 101 sec

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Page 1

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OM protein - protein search, using sw model

Run on: December 13, 2001, 11:56:05 ; Search time 20.43 Seconds  
(without alignments)

8.812 Million cell updates/sec

Title: US-09-424-080A-2

Perfect score: 11

Sequence: 1 LXXXXXX 8

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 8027

Minimum DB seq length: 8

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: /cgn2.6/prodata/2/1aa/5A.COMB.pep.\*  
2: /cgn2.6/prodata/2/1aa/5B.COMB.pep.\*  
3: /cgn2.6/prodata/2/1aa/6A.COMB.pep.\*  
4: /cgn2.6/prodata/2/1aa/6B.COMB.pep.\*  
5: /cgn2.6/prodata/2/1aa/PCUTS.COMB.pep.\*  
6: /cgn2.6/prodata/2/1aa/Backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36.4	8	1	US-07-234-381A-1	Sequence 1, Appl
2	36.4	8	1	US-07-643-948A-1	Sequence 1, Appl
3	36.4	8	1	US-07-643-948A-3	Sequence 3, Appl
4	36.4	8	1	US-07-620-410-3	Sequence 3, Appl
5	36.4	8	1	US-07-780-081-1	Sequence 1, Appl
6	36.4	8	1	US-07-717-316B-4	Sequence 4, Appl
7	36.4	8	1	US-07-737-852-3	Sequence 3, Appl
8	36.4	8	1	US-07-621-670-6	Sequence 6, Appl
9	36.4	8	1	US-07-657-769B-10	Sequence 10, Appl
10	36.4	8	1	US-07-657-769B-40	Sequence 40, Appl
11	36.4	8	1	US-07-657-769B-50	Sequence 50, Appl
12	36.4	8	1	US-07-876-280-11	Sequence 11, Appl
13	36.4	8	1	US-07-729-513-3	Sequence 3, Appl
14	36.4	8	1	US-07-718-274A-16	Sequence 16, Appl
15	36.4	8	1	US-07-718-274A-49	Sequence 49, Appl
16	36.4	8	1	US-07-792-259-6	Sequence 6, Appl
17	36.4	8	1	US-07-830-330-4	Sequence 4, Appl
18	36.4	8	1	US-07-725-331-58	Sequence 58, Appl
19	36.4	8	1	US-07-626-589-12	Sequence 12, Appl
20	36.4	8	1	US-07-752-101A-4	Sequence 4, Appl
21	36.4	8	1	US-07-946-237-5	Sequence 5, Appl
22	36.4	8	1	US-07-946-237-6	Sequence 6, Appl
23	36.4	8	1	US-07-932-200-17	Sequence 17, Appl
24	36.4	8	1	US-07-820-154A-36	Sequence 36, Appl
25	36.4	8	1	US-07-920-519-9	Sequence 9, Appl
26	36.4	8	1	US-07-920-519-11	Sequence 11, Appl
27	36.4	8	1	US-08-057-184-11	Sequence 11, Appl

28	36.4	8	1	US-08-057-184-12	Sequence 12, Appl
29	36.4	8	1	US-07-872-644-25	Sequence 25, Appl
30	36.4	8	1	US-08-086-410-6	Sequence 6, Appl
31	36.4	8	1	US-08-086-410-8	Sequence 8, Appl
32	36.4	8	1	US-07-793-213D-70	Sequence 70, Appl
33	36.4	8	1	US-08-149-106-16	Sequence 16, Appl
34	36.4	8	1	US-08-149-106-49	Sequence 49, Appl
35	36.4	8	1	US-07-603-675-6	Sequence 6, Appl
36	36.4	8	1	US-07-808-317-4	Sequence 4, Appl
37	36.4	8	1	US-07-841-997A-7	Sequence 7, Appl
38	36.4	8	1	US-08-103-490A-6	Sequence 6, Appl
39	36.4	8	1	US-08-030-731A-12	Sequence 12, Appl
40	36.4	8	1	US-08-030-731A-23	Sequence 23, Appl
41	36.4	8	1	US-07-968-781A-53	Sequence 53, Appl
42	36.4	8	1	US-07-968-781A-57	Sequence 57, Appl
43	36.4	8	1	US-07-968-781A-61	Sequence 61, Appl
44	36.4	8	1	US-07-968-781A-61	Sequence 61, Appl
45	36.4	8	5	PCT-US94-05150-5	Sequence 5, Appl

#### ALIGNMENTS

RESULT 1  
US-07-234-381A-1  
Sequence 1, Application US/07234381A  
Patent No. 5185147  
GENERAL INFORMATION:  
APPLICANT: Papadimitriou, Lawrence D  
TITLE OF INVENTION: Short Polypeptide Sequences Useful In The Production  
TITLE OF INVENTION: And Detection Of Antibodies Against Human Immunodeficiency  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Elman, Gerry J  
STREET: 20 West Third Street  
STREET: P.O. Box 703  
CITY: Media  
STATE: PA  
COUNTRY: USA  
ZIP: 19063  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC-compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/234,381A  
FILING DATE: 19880819  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Elman, Gerry J.  
REGISTRATION NUMBER: 24,404  
REFERENCE/DOCKET NUMBER: C8-038  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215 892 9577  
TELEFAX: 215 892 9580  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-234-381A-1

Query Match 36.4%; Score 4; DB 1; Length 8  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
Db 2 L 2



RESULT 2  
US-07-643-948A-1  
Sequence 1, Application US/07643948A  
Patent No. 5200505  
GENERAL INFORMATION:  
APPLICANT: Kazutoh TAKESAKO et al.  
TITLE OF INVENTION: NO. 5200505el R106 Compounds  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Displaywrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/643,948A  
FILING DATE: 19910122  
CLASSIFICATION: 330  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek Jr.  
REGISTRATION NUMBER: 33,367  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: circular  
ORIGINAL SOURCE:  
ORGANISM: Aureobasidium  
FEATURE:  
NAME/KEY: modified-site  
LOCATION: 1  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note="MeVal"  
FEATURE:  
NAME/KEY: modified-site  
LOCATION: 3  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note="N-methylphenylalanine, B-hydroxy-N-methylphenylalanine or Phe"  
FEATURE:  
NAME/KEY: modified-site  
LOCATION: 5  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note="alle, Val or Leu"  
FEATURE:  
NAME/KEY: modified-site  
LOCATION: 6  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note="MeVal or Val"  
FEATURE:  
NAME/KEY: modified-site  
LOCATION: 8  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note="B-hydroxy-N-methylvaline, MeVal, Val,  
OTHER INFORMATION: methylvaline, gamma-hydroxy-N-methylphenylalanine,  
OTHER INFORMATION: N,B-dimethylaspartic acid, B-hydroxy-N-methylphenylalanine,  
OTHER INFORMATION: or N-methylphenylalanine."  
FEATURE:  
NAME/KEY: modified-site  
LOCATION: 8  
IDENTIFICATION METHOD:

OTHER INFORMATION: /note="N-methyl-2,3-  
OTHER INFORMATION: dihydrovaline or N-methyl-3,4-dihydrovaline."  
FEATURE:  
NAME/KEY: modified-site  
LOCATION: 8  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note="wherein the amino  
OTHER INFORMATION: acid has a substituent 2-hydroxy-3-methylbutanoic acid or  
OTHER INFORMATION: 2-hydroxy-3-methylpentanoic acid bound to location 1."  
US-07-643-948A-1  
Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred No. 1,3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 L 1  
DB 7 L 7  
RESULT 3  
US-07-643-948A-3  
Sequence 3, Application US/07643948A  
Patent No. 5200505  
GENERAL INFORMATION:  
APPLICANT: Kazutoh TAKESAKO et al.  
TITLE OF INVENTION: NO. 5200505el R106 Compounds  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Displaywrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/643,948A  
FILING DATE: 19910122  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek Jr.  
REGISTRATION NUMBER: 33,367  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: circular  
ORIGINAL SOURCE:  
ORGANISM: Aureobasidium  
FEATURE:  
NAME/KEY: modified-site  
LOCATION: 1  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note="MeVal"  
FEATURE:  
NAME/KEY: modified-site  
LOCATION: 3  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note="N-methylphenylalanine, Sarcosine, N-methylserine or  
OTHER INFORMATION: B-oxo-N-methylphenylalanine"  
FEATURE:  
NAME/KEY: modified-site

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Page 3

LOCATION: 5  
IDENTIFICATION METHOD: /note- "aile"  
OTHER INFORMATION: /note- "aile"  
FEATURE:  
NAME/KEY: modified-site  
LOCATION: 6  
IDENTIFICATION METHOD: /note- "meval"  
OTHER INFORMATION: /note- "meval"  
FEATURE:  
NAME/KEY: modified-site  
LOCATION: 8  
IDENTIFICATION METHOD: /note- "B-hydroxy-N-  
OTHER INFORMATION: methionine or Sarcosine, wherein the amino acid has a  
OTHER INFORMATION: substituent 2-hydroxy-3-methylpentanoic acid which is bound  
OTHER INFORMATION: to the amino acid in location 1 to form the cyclic peptide."  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION: /note- "Excluding wherein  
OTHER INFORMATION: location 3 is N-methylphenylalanine and location 8 is  
OTHER INFORMATION: B-hydroxy-N-methylvaline."  
US-07-643-948A-3

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
DB 7 L 7

RESULT 4  
US-07-620-410-3  
Sequence 3, Application US/07620410  
Patent No. 5217953  
GENERAL INFORMATION:  
APPLICANT: Gozes, Ilana  
APPLICANT: Breneman, Douglas E.  
APPLICANT: Fridkin, Mati  
TITLE OF INVENTION: A NOVEL VASOACTIVE INTESTINAL PEPTIDE  
TITLE OF INVENTION: ANTAGONIST  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESS: CUSHMAN, DABRY & CUSHMAN  
STREET: 1615 L Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/07/620,410  
APPLICATION NUMBER: US/07/620,410  
FILING DATE: 19901130  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Scott, Watson T.  
REFERENCE/DOCKET NUMBER: 26, 581  
WTS/5683/82679  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
TELEFAX: 248453 CUSH  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
US-07-620-410-3

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
DB 1 L 1

RESULT 5  
US-07-780-081-1  
Sequence 1, Application US/07780081  
Patent No. 5229366  
GENERAL INFORMATION:  
APPLICANT: TSUKADA, Yoshihisa  
APPLICANT: ORIKASA, Atsushi  
TITLE OF INVENTION: PEPTIDE-CONTAINING POLYETHYLENE GLYCOL  
TITLE OF INVENTION: DERIVATIVES AND APPLICATION THEREOF  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESS: Sughrue, Mion, Zinn, Macpeak and Seas  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/780,081  
FILING DATE: 19911021  
CLASSIFICATION: 530  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-293-7060  
TELEFAX: 202-293-7860  
TELEFAX: 6491103  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-780-081-1

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
DB 3 L 3

RESULT 6  
US-07-717-316B-4  
Sequence 4, Application US/07717316B  
Patent No. 5229495  
GENERAL INFORMATION:  
APPLICANT: Ichijo, Hiromori, Miyazono, Kohel  
APPLICANT: Rinsarand, Lars, Hellman, Ols, Wernstedt, Christer  
APPLICANT: Heidin, Carl-Henrik  
TITLE OF INVENTION: Substantially pure Receptor-Like

TITLE OF INVENTION: TGF- $\alpha$ 1 Binding Molecules And Uses Thereof  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felte & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/717,316B  
FILING DATE: 19910618  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5229495man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 259  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 688-3884  
INFORMATION FOR SEQ ID NO.: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-717-316B-4

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
DB 6 L 6

RESULT 7  
US-07-737-852-3  
Sequence 3, Application US/07737852  
Patent No. 5243027  
GENERAL INFORMATION:  
APPLICANT: Mimura, Tsutomu  
APPLICANT: Kobama, Kazuhiko  
APPLICANT: Tsutsumi, Ryohichi  
TITLE OF INVENTION: ANGIOGENIN CONVERTING ENZYME  
TITLE OF INVENTION: INHIBITOR  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sughrue, Mion, Zimo, Macpeak & Seas  
STREET: 2100 Pennsylvania Avenue  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/737,852  
FILING DATE: 19910731  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 02-46975

FILING DATE: 26-FEB-1990  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO.: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Bacillus stearothermophilus  
STRAIN: NCA-1503  
US-07-737-852-3

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1  
DB 8 L 8

RESULT 8  
US-07-621-670-6  
Sequence 6, Application US/07621670  
Patent No. 5254801  
GENERAL INFORMATION:  
APPLICANT: Dolson, Stanton B.  
TITLE OF INVENTION: Heterologous Dominant Conditional Lethal  
TITLE OF INVENTION: Genes and Use Thereof  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dennis R. Hoerner, Jr. Monsanto Co. BBAP  
STREET: 700 Chesterfield Village Parkway  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/621,670  
FILING DATE: 19901203  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoerner Jr., Dennis R.  
REGISTRATION NUMBER: 30,914  
REFERENCE/DOCKET NUMBER: 38-21(10523)A  
TELEPHONE: (314)537-6047  
TELEFAX: (314)537-6099  
INFORMATION FOR SEQ ID NO.: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-621-670-6

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1

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Db 3 L 3

RESULT 9

US-07-657-769B-10  
Sequence 10, Application US/07657769B

Patent No. 5256766

GENERAL INFORMATION:

APPLICANT: COUGHLIN, SHAUN R.  
TITLE OF INVENTION: RECOMBINANT RECEPTOR AND RELATED

NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:

ADDRESSEE: IRELL & MANELLA  
STREET: 545 MIDDLEFIELD ROAD, SUITE 200

CITY: MENLO PARK  
STATE: CA

COUNTRY: USA  
ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/657,769B

FILING DATE: 19910219  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 2000-0502.00

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-327-7250

TELEFAX: 415-327-2951  
TELEX: 706141

INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids  
TYPE: AMINO ACID

STRANDEDNESS: single  
TOPOLOGY: linear

US-07-657-769B-10

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1

Db 3 L 3

RESULT 10

US-07-657-769B-40  
Sequence 40, Application US/07657769B

Patent No. 5256766

GENERAL INFORMATION:

APPLICANT: COUGHLIN, SHAUN R.  
TITLE OF INVENTION: RECOMBINANT RECEPTOR AND RELATED

NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:

ADDRESSEE: IRELL & MANELLA  
STREET: 545 MIDDLEFIELD ROAD, SUITE 200

CITY: MENLO PARK  
STATE: CA

COUNTRY: USA  
ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/657,769B

FILING DATE: 19910219

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 2000-0502.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-327-7250

TELEFAX: 415-327-2951

TELEX: 706141

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

US-07-657-769B-50

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/657,769B

FILING DATE: 19910219  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 2000-0502.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-327-7250

TELEFAX: 415-327-2951

TELEX: 706141

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

US-07-657-769B-40

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1

Db 3 L 3

RESULT 11

US-07-657-769B-50  
Sequence 50, Application US/07657769B

Patent No. 5256766

GENERAL INFORMATION:

APPLICANT: COUGHLIN, SHAUN R.  
TITLE OF INVENTION: RECOMBINANT RECEPTOR AND RELATED

NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:

ADDRESSEE: IRELL & MANELLA  
STREET: 545 MIDDLEFIELD ROAD, SUITE 200

CITY: MENLO PARK  
STATE: CA

COUNTRY: USA  
ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/657,769B

FILING DATE: 19910219

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 2000-0502.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-327-7250

TELEFAX: 415-327-2951

TELEX: 706141

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

US-07-657-769B-50

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
Db 3 L 3

## RESULT 12

US-07-876-280-11  
; Sequence 11, Application US/07876280  
; Patent No. 5262158  
; GENERAL INFORMATION:  
; APPLICANT: Payne, Jewel M.  
; APPLICANT: Cannon, Raymond J. C.  
; APPLICANT: Bagley, Angela L.  
; TITLE OF INVENTION: No. 5262158: Bacillus thuringiensis isolates for  
; TITLE OF INVENTION: Controlling Acarides  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/876,280  
; FILING DATE: 19920430  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: M/S 104  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-876-280-11

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
Db 7 L 7

RESULT 13  
US-07-729-513-3  
; Sequence 3, Application US/07729513  
; Patent No. 5270175  
; GENERAL INFORMATION:  
; APPLICANT: Moll, Benjamin A.  
; TITLE OF INVENTION: Methods and Compositions for Producing  
; TITLE OF INVENTION: Metabolic Products from Algae  
; NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:  
ADDRESSEE: James M. Heslin  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 96301

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/729,513  
FILING DATE: 19910712  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Heslin, James M.  
REGISTRATION NUMBER: 29,541  
REFERENCE/DOCKET NUMBER: 12176-21/A0118  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-729-513-3

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
Db 7 L 7

## RESULT 14

US-07-718-274A-16  
; Sequence 16, Application US/07718274A  
; Patent No. 5284756  
; GENERAL INFORMATION:  
; APPLICANT: Glina, Lynn  
; APPLICANT: Parsons, Thomas F.  
; APPLICANT: Theofan, Georgia  
; TITLE OF INVENTION: Osteogenic Factor  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; STREET: Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/718,274A  
; FILING DATE: 19910620  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/415,555  
; FILING DATE: 04-OCT-1989

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/256,034  
FILING DATE: 11-OCT-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharp, Jeffrey S.  
REGISTRATION NUMBER: 31,879  
REFERENCE/DOCKET NUMBER: 27129/9430  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-718-274A-16

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
Db 1 L 1

RESULT 15  
US-07-718-274A-49  
Sequence 49, Application US/07718274A  
Patent No. 5284756  
GENERAL INFORMATION:  
APPLICANT: Grilina, Lynn  
APPLICANT: Parsons, Thomas F.  
APPLICANT: Theofan, Georgia  
TITLE OF INVENTION: Osteogenic Factor  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: Two First National Plaza, 20 South Clark  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/718, 274A  
FILING DATE: 19910620  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/415,555  
FILING DATE: 04-OCT-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/256,034  
FILING DATE: 11-OCT-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharp, Jeffrey S.  
REGISTRATION NUMBER: 31,879  
REFERENCE/DOCKET NUMBER: 27129/9430  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-718-274A-49

Query Match 36.4%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 L 1  
Db 8 L 8

Search completed: December 13, 2001, 11:56:06  
Job time: 30 sec

=> fil reg

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STRUCTURE FILE UPDATES: 11 DEC 2001 HIGHEST RN 374745-93-4  
DICTIONARY FILE UPDATES: 11 DEC 2001 HIGHEST RN 374745-93-4

TSCA INFORMATION NOW CURRENT THROUGH July 7, 2001

Please note that search-term pricing does apply when  
conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Calculated physical property data is now available. See HELP PROPERTIES  
for more information. See STNote 27, Searching Properties in the CAS  
Registry File, for complete details:  
<http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf>

=> d sta que l4

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L2 896 SEA FILE=REGISTRY ABB=ON PLU=ON L[TRQMEG][ERDLIA][KRNMS][KRD  
NS][YH][SRDNA][PRDL]/SQSP  
L3 2 SEA FILE=REGISTRY ABB=ON PLU=ON L2 AND 8/SQL  
L4 2 SEA FILE=REGISTRY ABB=ON PLU=ON (L1 OR L3)

=> d his l4-

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SAV L4 JAMROZ424/A

FILE 'HCAOLD' ENTERED AT 12:31:09 ON 13 DEC 2001  
L5 0 S L4

FILE 'USPATFULL' ENTERED AT 12:31:15 ON 13 DEC 2001  
L6 0 S L4

FILE 'HCAPLUS' ENTERED AT 12:31:17 ON 13 DEC 2001  
L7 1 S L4

FILE 'REGISTRY' ENTERED AT 12:31:37 ON 13 DEC 2001

=> d sqide can tot l4

L4 ANSWER 1 OF 2 REGISTRY COPYRIGHT 2001 ACS  
RN 216579-44-1 REGISTRY  
CN L-Arginine, L-leucyl-L-arginyl-L-arginyl-L-arginyl-L-arginyl-L-histidyl-L-  
arginyl- (9CI) (CA INDEX NAME)  
FS PROTEIN SEQUENCE; STEREOSEARCH  
SQL 8

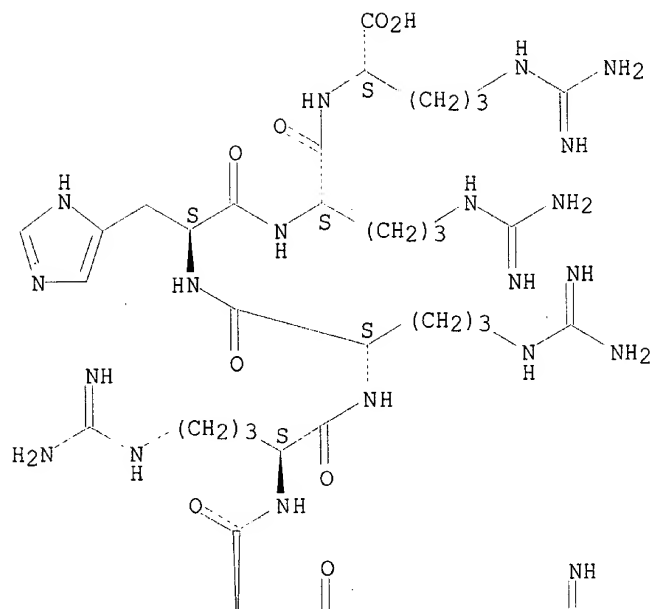
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SR CA  
LC STN Files: CA, CAPLUS, TOXCENTER, TOXLIT

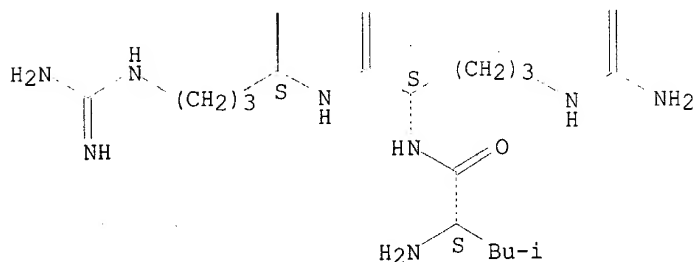
Absolute stereochemistry.

Point of Contact:  
Jan Delaval  
Librarian-Physical Sciences  
CM1 1E04 Tel: 308-4498

PAGE 1-A



PAGE 2-A



1 REFERENCES IN FILE CA (1967 TO DATE)  
 1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA  
 1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 130:33014

L4 ANSWER 2 OF 2 REGISTRY COPYRIGHT 2001 ACS  
 RN 216579-39-4 REGISTRY  
 CN L-Proline, L-leucyl-L-threonyl-L-.alpha.-glutamyl-L-lysyl-L-lysyl-L-tyrosyl-L-seryl- (9CI) (CA INDEX NAME)  
 FS PROTEIN SEQUENCE; STEREOSEARCH  
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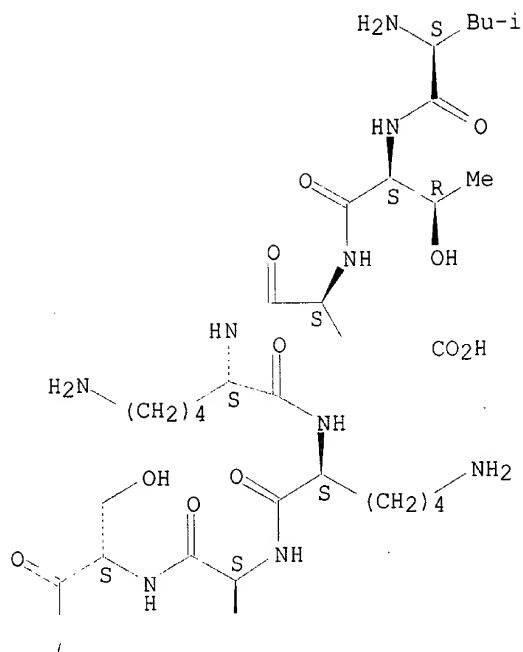
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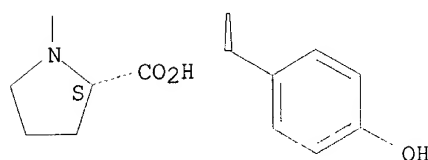
Absolute stereochemistry.



PAGE 1-A



PAGE 2-A



1 REFERENCES IN FILE CA (1967 TO DATE)  
 1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA  
 1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 130:33014

=> fil hcaplus

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FILE COVERS 1947 - 13 Dec 2001 VOL 135 ISS 25

FILE LAST UPDATED: 11 Dec 2001 (20011211/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

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=> d all 17

L7 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2001 ACS  
 AN 1998:789037 HCAPLUS  
 DN 130:33014  
 TI Compositions for enhancing immunosuppressants pharmaceutical activities  
 IN Zavialov, Vladimir Petrovich; Vasilenko, Raisa Nikolaevna; Dolgikh, Dmitry Aleksandrovich; Kirpichnikov, Mikhail Petrovich; Navolotskaya, Elena Vitalievna; Korpela, Timo Kalevi  
 PA Russia  
 SO PCT Int. Appl., 26 pp.  
 CODEN: PIXXD2  
 DT Patent  
 LA English  
 IC ICM A61K038-04  
 ICS A61K038-13; A61K038-21  
 CC 1-7 (Pharmacology)  
 Section cross-reference(s): 15  
 FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9852594	A1	19981126	WO 1998-FI418	19980518
W:			AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM	
RW:			GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG	
FI 9702121	A	19981120	FI 1997-2121	19970519
AU 9874352	A1	19981211	AU 1998-74352	19980518
EP 981359	A1	20000301	EP 1998-921528	19980518
R:			AT, DE, ES, FR, GB, IT, SE, FI	
PRAI FI 1997-2121		19970519		
WO 1998-FI418		19980518		
AB			The present invention provides compns. for efficient amplification of immunosuppressive activity of cyclosporins, FK506 or rapamycin to decrease therapeutical dose of immunosuppressants and, as a consequence, avoidance of their undesirable side effects during organ and tissue transplantation, and treatment of different diseases. These compns. include cyclosporins, FK506 or rapamycin and biol. active peptides corresponding to the high-affinity binding/anti-lymphoproliferative site of IFNs-a,b,w,t, or recombinant proteins having the amino acid sequences corresponding to the said site.	
ST			immunosuppressant adjuvant formulation peptide	
IT			Interferon .tau. Interferon .alpha. Interferon .beta. RL: PRP (Properties) (antilymphoproliferative site of; compns. for enhancing immunosuppressant pharmaceutical activities)	
IT			Adenocarcinoma inhibitors Anti-inflammatory drugs Antirheumatic drugs Autoimmune diseases Drug bioavailability Immunosuppressants	

Leukemia inhibitors  
Lupus erythematosus  
Lymphoma inhibitors  
Myasthenia gravis  
Psoriasis  
Transplant (organ)  
Uveitis  
    (compns. for enhancing immunosuppressant pharmaceutical activities)

IT Interferon .alpha.2  
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BIOL (Biological study); PROC (Process)  
    (compns. for enhancing immunosuppressant pharmaceutical activities)

IT Peptides, biological studies  
RL: PEP (Physical, engineering or chemical process); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)  
    (compns. for enhancing immunosuppressant pharmaceutical activities)

IT Interferons  
RL: PRP (Properties)  
    (interferon .omega., antilymphoproliferative site of; compns. for enhancing immunosuppressant pharmaceutical activities)

IT Antitumor agents  
    (myeloma; compns. for enhancing immunosuppressant pharmaceutical activities)

IT 216579-39-4D, analogs 216579-44-1D, analogs  
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BIOL (Biological study); PROC (Process)  
    (compns. for enhancing immunosuppressant pharmaceutical activities)

IT 53123-88-9, Rapamycin 79217-60-0D, Cyclosporin, derivs. 104987-11-3, Fk506  
RL: PEP (Physical, engineering or chemical process); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)  
    (compns. for enhancing immunosuppressant pharmaceutical activities)

RE.CNT 5  
RE  
    (1) University of Florida; WO 9009806 A2 1990 HCAPLUS  
    (2) University of Florida; WO 9410313 A2 1994 HCAPLUS  
    (3) Vacsyn, S; FR 2706772 A1 1994 HCAPLUS  
    (4) Zarogoulidis, K; Lung Cancer 1996, V15(2), P197 MEDLINE  
    (5) Zav'Yalov, V; Mol Immunol 1995, V32(6), P425 HCAPLUS

7/7/2 (Item 2 from file: 73)  
DIALOG(R)File 73:EMBASE  
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06929781 EMBASE No: 1997214260  
**Structure-activity of type I interferons**  
Viscomi G.C.  
G.C. Viscomi, Alfa Wassermann, Dept. of Biotechnology/Immunology, Via  
Ragazzi Del '99 N.5, 40133 Bologna Italy  
Biotherapy ( BIOTHERAPY (THE NETHERLANDS) ) (Netherlands) 1997, 10/1  
(59-86)  
CODEN: BTHRE ISSN: 0921-299X  
DOCUMENT TYPE: Journal; Review  
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH  
NUMBER OF REFERENCES: 126

Type I IFNs constitute a family of proteins exhibiting high **homology** in primary, secondary, and tertiary structures. They interact with the same receptor and transmit signals to cellular nucleus through a similar mechanism, eliciting roughly homogeneous biological activity. Nevertheless, the members of that family, IFNalpha species, IFNbeta and IFNomega, due to local differences in the structure sometime show distinct properties. From the reported data it results that even minute changes or differences in the primary sequences could be responsible for a significant variety of biological actions, thus inducing to the hypothesis that Type I IFNs, rather than to be the result of a redundant replication during the evolution, play definite roles in the defense of living organisms to foreign agents.

7/7/3 (Item 3 from file: 73)  
DIALOG(R)File 73:EMBASE  
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06064616 EMBASE No: 1995095061  
**Human type I interferons: Structure and function**  
Kontsek P.  
Institute of Virology, Slovak Academy of Sciences, Dubravska cesta 9,942  
46 Bratislava Slovakia  
Acta Virologica ( ACTA VIROL. ) (Czech Republic) 1994, 38/6 (345-360)  
CODEN: AVIRA ISSN: 0001-723X  
DOCUMENT TYPE: Journal; Review  
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

**Human type I interferons** (IFNs) comprise a family of 13 IFN-alpha subtypes and single species of IFN-beta and IFN-omega. Their 20% overall sequence **homology** determines identical secondary and tertiary folding of polypeptides. Three-dimensional models suggest that the globular structure of type I IFNs consists of a bundle of 5 alpha-helices, which might form two polypeptide domains. Disulfide bond Cys 29-Cys 139 stabilizes both domains in a bioactive configuration. The IFN molecule exerts its functional entity only as an organic polypeptide complex and therefore molecular fragments apparently lack biological activity. IFN-beta, IFN-omega and some IFN-alpha subtypes are glycoproteins, but the sugar moiety was found to be neither structurally nor functionally relevant. Type I IFNs share a common cellular receptor, a fact that implies a high structural conservativity of their receptor-binding areas. Two conservative hydrophilic regions associated with the amino acids (aa) 30-41 and 120-145 appear to constitute the basic framework of receptor recognition site in type I IFNs. However, the individual IFN-(sub)types induce different spectra of biological effects which reflect some specificity in modelling of binding sites. Besides a subtle sequential heterogeneity in the segments aa 30-41 and 120-145, also the variable hydrophilic aa regions 23-26, 68-85 and 112-121 are responsible for structural and functional individuality among human type I IFNs. The interaction between IFN and its receptor seems to be a complex event which triggers simultaneously antiviral, antiproliferative and immunomodulating actions, although different parts of

rocessing  
 2055349 TYPE  
 2597795 I  
 282134 INTERFERON?  
 2791 TYPE(W)I(W)INTERFERON?  
 2995840 REVIEW?  
 S5 152 TYPE(W)I(W)INTERFERON? AND REVIEW?

?rd s5  
 ...examined 50 records (50)  
 ...examined 50 records (100)  
 ...examined 50 records (150)  
 ...completed examining records  
 S6 106 RD S5 (unique items)

?s s6 and homology  
 106 S6  
 237758 HOMOLOGY  
 S7 3 S6 AND HOMOLOGY

?t s7/7/all

7/7/1 (Item 1 from file: 73)  
 DIALOG(R)File 73:EMBASE  
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10784174 EMBASE No: 2000265957  
**HIV-1 gp41 and type I interferon. Sequence homology and biological as well as clinical implications**

Chen Y.-H.; Xiao Y.; Dierich M.P.  
 Prof. Y.-H. Chen, Laboratory of Immunology, Res. Centre Medical Research,  
 Tsinghua University, Beijing 100084 China  
 Immunologic Research ( IMMUNOL. RES. ) (United States) 2000, 22/1  
 (61-66)  
 CODEN: IMRSE ISSN: 0257-277X  
 DOCUMENT TYPE: Journal; Review  
 LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH  
 NUMBER OF REFERENCES: 38

HIV-1 gp41-like human **type I interferon** (IFN) could inhibit lymphocyte proliferation and up-modulate MHC class I and II and ICAM-1 molecule expression. Sequence comparison indicates that a similar epitope RILAV-YLKD exists between N-domain of gp41 and two regions in IFN-alpha (aa29-35 and 113-129), IFN-beta (aa31-37 and 125-138) and IFN-omega (aa29-35 and 123-136), which was shown to form IFN-alpha/beta-receptor binding site. Weak sequence similarity was also found to exist in both regions on gp41 and type I IFN of murine and bovine. Experimental studies indicated that a common immunological epitope exists between gp41 and IFN-alpha and -beta. Antibodies against human IFN-alpha and -beta recognized the common immunological epitope and inhibited gp41-binding to the potential cellular receptor protein p45. Moreover, the polyclonal antibody to IFN-beta completely inhibited gp41-binding to human T, B cells and monocytic cells, while IFN-alpha could only inhibit this binding incompletely. It was interestingly observed that human IFN-beta after preincubating with cells could incompletely inhibit the binding of gp41 to human B cells and monocytic cells, and very weakly inhibit the binding to human T cells, indicating that the receptor for IFN-beta-binding may be involved in gp41 binding. This potential relationship may be based on the amino acid sequence **homology** in the receptor binding region between gp41 and IFN-beta. It was observed that the increased levels of antibodies against human IFN-alpha and -beta exist in HIV-1-infected individuals and are associated with the common epitope on gp41. Besides, several studies provided experimental evidence that the common immunological epitope could induce protective activity against HIV-1. The IFN-alpha-based vaccine has showed a significant reduction of disease progression in IFN-alpha-vaccine-treated HIV-infected patients. Recent experimental evidence indicates that gp41 and IFN-beta were involved in downregulation of CCR5 expression and induction of cell activation or signal transduction. Whether it may be performed by a similar mechanism is still to be investigated.

IFN molecule are not involved equally in eliciting of respective basal activities.  
?ds

Set	Items	Description
S1	0	(INTERFERON?AND ALBEFERON)
S2	0	(INTEFERON?) AND ALBEFERON?
S3	14	INTERFERON? AND <u>ALBEFERON?</u> <i>DUP REM</i>
S4	9	<u>RD S3</u> (unique items)
S5	152	TYPE(W) I(W) INTERFERON? (AND REVIEW?
S6	106	RD S5 (unique items)
S7	3	S6 AND <u>HOMOLOGY</u>
?		

that albebetin possesses the properties of the molten globule state. Grafting of the octapeptide to the N-terminus of this de novo protein affects its structure. We show here that **albeferon** maintains a secondary s content of albebetin; it becomes more compact and much more stable toward urea-induced unfolding as compared to albebetin and even possesses some weak tertiary structure (at least around Tyr!7). This means that the structure of the artificial protein albebetin can be improved by a simple procedure of octapeptide grafting to its N-terminus.

4/7/6 (Item 6 from file: 5)  
DIALOG(R)File 5:Biosis Previews(R)  
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11277016 BIOSIS NO.: 199800058348  
**Synthetic octapeptide alpha-peptoferon and de novo protein albeferon have the same anti-proliferative activity as human interferon alpha2.**  
AUTHOR: Zav'yalov V P(a); Vasilenko R N(a); Navolotskaya E V(a); Dolgikh D P(a); Kirpichnikov M P; Abramov V M(a)  
AUTHOR ADDRESS: (a)Inst. Immunol. Eng., Lyubuchany\*\*Russia  
JOURNAL: Journal of Interferon and Cytokine Research 17 (SUPPL. 2):pS99 Oct., 1997  
CONFERENCE/MEETING: Annual Meeting of the International Society for Interferon and Cytokine Research San Diego, California, USA October 19-24, 1997  
SPONSOR: International Society for Interferon and Cytokine Research  
ISSN: 1079-9907  
RECORD TYPE: Citation  
LANGUAGE: English

4/7/7 (Item 7 from file: 5)  
DIALOG(R)File 5:Biosis Previews(R)  
(c) 2001 BIOSIS. All rts. reserv.

10921786 BIOSIS NO.: 199799542931  
**Interferons alpha/beta and their receptors: Place in the hierarchy of cytokines.**  
AUTHOR: Zav'yalov Vladimir P(a); Zav'yalova Galina A  
AUTHOR ADDRESS: (a)Inst. Immunological Engineering, 142380 Lyubuchany, Moscow Region\*\*Russia  
JOURNAL: APMIS 105 (3):p161-186 1997  
ISSN: 0903-4641  
RECORD TYPE: Abstract  
LANGUAGE: English

ABSTRACT: **Interferons** alpha/beta (IFNs-alpha/beta) are the first cytokines to be produced by recombinant DNA technology. They regulate growth and differentiation, affecting cellular communication, signal transduction pathways and immunological control. This review focuses on the relationships between the structure and biological activities of IFNs-alpha/beta induced as a result of specific interactions with different types of polypeptide receptors as well as on the role of glycolipids in the modulation of these activities. The discovery of the primary structure homology of HuIFNs-alpha and thymus hormone-thymosin alpha-1 (TM-alpha-1), the experimental finding of the competition between IFN-alpha and TM-alpha-1 for common receptors and the reproduction by reHuIFN-alpha-2 of TM-alpha-1 immunomodulating activities create the basis of reHuIFN-alpha therapeutics instead of TM-alpha-1 and potentiation of vaccines by reHuIFN-alpha. The first successful attempt at grafting of the HuIFN-alpha-2s TM-alpha-1-like immunomodulating site to the designed de novo protein **albeferon** is described. This article also aims at reviewing recent data concerning the structure of other cytokines and their receptors. Their reciprocal structure-function taxonomy is proposed. The place of IFNs-alpha/beta and their receptors in the hierarchy of cytokines is determined.

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Thanks and happy holidays.

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